

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: August 1, 2005, 08:34:29 ; Search time 39 Seconds  
(without alignments)  
29.605 Million cell updates/sec

Title: US-10-663-749-18  
Perfect score: 62  
Sequence: 1 GIEALPRTMSQ 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : PIR79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	500	1 JC2231	prostaglandin-I sy
2	41	66.1	500	2 AS3658	prostaglandin-I sy
3	40	64.5	880	2 T04523	hypothetical prote
4	39	62.9	367	2 D85727	oxygen sensing pro
5	39	62.9	367	2 E90890	oxygen sensing pro
6	39	62.9	838	2 JC7363	95K retinoblastoma
7	38	61.3	442	2 B75634	hypothetical prote
8	38	61.3	597	2 S40998	hypothetical prote
9	38	61.3	893	2 G88551	protein M01A6.2 (i
10	38	61.3	2022	2 T43214	ovrl protein - nem
11	37	57.7	160	2 D83156	molybdopterin bios
12	37	59.7	264	2 H81834	hypothetical prote
13	36	58.1	450	2 AP2962	aminotransferase f
14	36	58.1	450	2 H98320	family II aminotra
15	36	58.1	507	2 S52469	SOX9 protein - mou
16	36	58.1	509	2 A55204	transcription fact
17	36	58.1	739	2 T10932	polynucleotide
18	36	58.1	854	2 D82324	conserved hypothet
19	35	56.5	470	2 A87547	vanillin dehydroge
20	35	56.5	479	1 T46576	phosphoprotein pho
21	35	56.5	575	2 T13094	beta-fructofuranos
22	35	56.5	593	2 T01575	hypothetical prote
23	35	56.5	593	2 S76615	hypothetical prote
24	35	56.5	683	2 T24486	hypothetical prote
25	35	56.5	703	2 B97123	polynucleotide
26	35	56.5	727	2 A71069	hypothetical prote
27	35	56.5	741	2 H90607	atp-dependent prote
28	35	56.5	748	2 D84595	PEARL 4 protein f
29	35	56.5	807	2 D64902	hypothetical prote

30	56.5	1498	2 AF1082	B. subtilis Yuka p
31	55.6	581	2 T12095	beta-fructofuranos
32	54.8	157	2 A40323	rodletless protein
33	54.8	212	2 T25905	hypothetical prote
34	54.8	295	2 E70022	transcription regu
35	54.8	351	2 A12325	hypothetical prote
36	54.8	354	2 D96522	ornithine cyclodaa
37	54.8	356	2 S32049	1-deoxy-D-xylulose
38	54.8	379	2 C81578	cr071 hypothetical
39	54.8	379	2 B72091	hypothetical prote
40	54.8	379	2 G86533	CT071 hypothetical
41	54.8	389	2 T20604	hypothetical prote
42	54.8	397	2 G90048	hypothetical prote
43	54.8	427	2 AH0728	probable membrane
44	54.8	584	2 A49596	genome polypeptid
45	54.8	587	2 S58319	hypothetical prote
46	54.8	631	2 T07670	probable protein k
47	54.8	643	2 AC2199	phosphoenolpyruvat
48	54.8	671	2 A56592	MDPH-ferrithemopro
49	54.8	682	2 D84579	probable Tail-1like
50	54.8	799	2 S75351	hypothetical prote
51	54.8	815	2 H84139	dihydropterolate sy
52	54.8	1065	2 S19482	hypothetical prote
53	54.8	2504	2 A57788	enoyl-l-acyl-carrie
54	54.8	5138	2 B96695	hypothetical prote
55	53.2	171	2 T48359	hypothetical prote
56	53.2	264	2 B81127	probable gufa prot
57	53.2	269	2 G12550	hypothetical prote
58	53.2	270	2 B75259	end-xyloglucan tra
59	53.2	277	2 J80156	urate oxidase (EC
60	53.2	301	2 S38910	urate oxidase (EC
61	53.2	308	2 S38911	hypothetical prote
62	53.2	313	2 A13173	conserved hypotet
63	53.2	348	2 B03328	probable pyridoxal
64	53.2	364	2 A81331	hypothetical prote
65	53.2	384	2 C66484	phosphorylase kina
66	53.2	388	1 S00731	probable lyase - S
67	53.2	403	2 T16073	arcentic efflux pum
68	53.2	431	2 A15599	omega-amino acid-p
69	53.2	439	2 B87638	glutamate-ammonia
70	53.2	454	2 T47127	nttc protein - Rho
71	53.2	455	2 S43175	glutamate reductase
72	53.2	501	1 S46591	hypothetical prote
73	53.2	514	2 D89775	hypothetical prote
74	53.2	523	2 T25998	hypothetical prote
75	53.2	525	2 T25900	hypothetical prote
76	53.2	542	2 T28688	hypothetical prote
77	53.2	736	1 M4XR3D	structural protein
78	53.2	746	2 H95340	probable cation tr
79	53.2	767	2 T42974	ribonucleoside-dip
80	53.2	810	2 S69652	hypothetical prote
81	53.2	880	2 D89756	protein T3EF7.2b f
82	53.2	950	2 S27473	protein T3EF7.2b f
83	53.2	1356	2 A54445	URSL1 protein - am
84	53.2	1487	2 T02850	janusin precursor,
85	53.2	1583	2 T082137	hypothetical prote
86	53.2	2442	2 T08621	hypothetical prote
87	52.4	725	2 A47168	centriosome associa
88	52.4	725	2 B82412	cardiac morphogene
89	51.6	118	1 S30566	hypothetical prote
90	51.6	122	2 T52544	beta-2-microglobul
91	51.6	164	1 G65085	hydrogenase 2 matu
92	51.6	164	2 F91115	hydrogenase 2 matu
93	51.6	164	2 F85958	probable processin
94	51.6	192	2 JC1354	pharomone biosynth
95	51.6	216	2 AB2582	glutamine amidotra
96	51.6	221	2 H97363	amidotransferase h
97	51.6	232	2 A83794	two-component resp
98	51.6	233	2 S52461	hypothetical prote
99	51.6	233	2 S53104	hypothetical prote
100	51.6	233	2 S38228	hypothetical prote
101	51.6	263	2 T01602	probable thiamin p
102	51.6	264	2 B86159	hypothetical prote



A:Accession: T04523  
A:Molecule type: DNA  
A:Residues: 1-880 <BEV>  
A:Cross-references: UNIPROT:Q9SVU3; EMBL:AL035353  
A:Experimental source: cultivar Columbia; BAC clone F16A16  
C:Genetics:  
A:Map position: 4  
A:Introns: 660/1  
A>Note: F16A16.130

Query Match 64.5%; Score 40; DB 2; Length 880;  
Best Local Similarity 60.0%; Pred. No. 25;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1EALPRTHE 10  
Db 44 G1EALPRTHE 53

RESULT 4  
D85727  
oxygen sensing protein [similarity] - Escherichia coli (strain O157:H7, substrain EDL933)  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Aug-2004  
C:Accession: D85727  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
11ler, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamoula, K.; Apodaca,  
Nature 409, 529-533, 2001  
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: D85727  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-367 <STO>  
A:Cross-references: UNIPROT:O8XAU8; GB:AE005174; NID:G12515189; PIDN:AA656280.1; GSPDB:C  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: 22221  
C:Superfamily: Oxygen sensor diguanylate cyclase/c-di-GMP phosphodiesterase

Query Match 62.9%; Score 39; DB 2; Length 367;  
Best Local Similarity 66.7%; Pred. No. 15;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 G1EALPRTHE 12  
Db 142 G1EALPRTHE 153

RESULT 5  
E90890  
oxygen sensing protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050  
C:Species: Escherichia coli  
C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 16-Aug-2004  
C:Accession: E90890  
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MUID:21156231; PMID:11258766  
A:Accession: E90890  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-367 <HAY>  
A:Cross-references: UNIPROT:O8XAU8; GB:BA000007; PIDN:BA35516.1; PID:G13361559; GSPDB:C  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: EC6293  
C:Superfamily: Oxygen sensor diguanylate cyclase/c-di-GMP phosphodiesterase

Query Match 62.9%; Score 39; DB 2; Length 367;  
Best Local Similarity 66.7%; Pred. No. 15;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 G1EALPRTHE 12  
Db 142 G1EALPRTHE 153

RESULT 6  
JC7363  
95K retinoblastoma protein-binding protein - human  
C:Species: Homo sapiens (man)  
C>Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 09-Jul-2004  
C:Accession: JC7363  
R:Men, H.; Ao, S.  
Biochem. Biophys. Res. Commun. 275, 141-148, 2000  
A>Title: RBP95, a novel leucine zipper protein, binds to the retinoblastoma protein.  
A:Reference number: JC7363  
A:Contents: Fetal brain  
A:Accession: JC7363  
A:Molecule type: mRNA  
A:Residues: 1-838 <MEN>  
A:Cross-references: UNIPROT:Q9HC82; GB:AF122819  
C:Comment: This protein, a member of retinoblastoma protein-associated protein and a leu  
ase II-mediated transcription and/or transcriptional processing.  
C:Genetics:  
A:Gene: rbp95  
A:Map position: 16p11.2-16p11.1  
C:Keywords: leucine zipper; transcription regulation

Query Match 62.9%; Score 39; DB 2; Length 838;  
Best Local Similarity 72.7%; Pred. No. 36;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 1EALPRTHE 12  
Db 105 1EALPRTHE 115

RESULT 7  
B75634  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: B75634  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
S.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
Science 286, 1571-1577, 1999  
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: B75634  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-442 <WHI>  
A:Cross-references: UNIPROT:Q9RZ14; GB:AE001826; NID:G6460827; PIDN:AA12621.1; PID:G646  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR80144  
A:Map position: megaplasmid  
A:Genome: plasmid  
A>Note: plasmid MP1

Query Match 61.3%; Score 38; DB 2; Length 442;  
Best Local Similarity 66.7%; Pred. No. 28;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 1EALPRTHE 10  
Db 88 1EALPRTHE 96

RESULT 8  
S40998  
hypothetical protein M01A8.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C/Accession: S40998  
R/Hawkins, T.; Thomas, K.  
Submitted to the EMBL Data Library, October 1993  
A/Reference number: S40997  
A/Accession: S40998  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-597 <HAW>  
A/Cross-references: EMBL:Z27081  
C/Genetics:  
A/Intons: 40/3; 76/1; 125/1; 199/1; 240/1; 274/1; 292/3; 392/3; 429/2; 486/2; 521/1

Query Match 61.3%; Score 38; DB 2; Length 597;  
Best Local Similarity 54.5%; Pred. No. 39;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IEALPRTHEQ 12  
:|:|:|:|:  
Db 282 VESLQKTHETQ 292

RESULT 9  
G88551  
protein M01A8.2 [imported] - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C/Accession: G88551  
R/Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A/Reference number: A75000; MUID:99069613; PMID:9851916  
A/Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A/Accession: G88551  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-893 <STO>  
A/Cross-references: UNIPROT:P34531; GB:chr\_III; PIDD:CAA81607.1; PID:g3878558; GSPDB:GNC  
C/Genetics:  
A/Gene: M01A8.2  
A/Map position: 3

Query Match 61.3%; Score 38; DB 2; Length 893;  
Best Local Similarity 54.5%; Pred. No. 60;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IEALPRTHEQ 12  
:|:|:|:|:  
Db 578 VESLQKTHETQ 588

RESULT 10  
T43214  
ovtl protein - nematode (Onchocerca volvulus)  
N/Alternate names: myosin-like antigen  
C/Species: Onchocerca volvulus  
C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C/Accession: T43214; A44939; A54513; S27825  
R/Tittertrapab, S.; Ritchie, T.L.; Tuan, R.S.; Shepley, K.J.; Dinman, J.D.; Neubert, T.  
Mol. Biochem. Parasitol. 69, 161-171, 1995  
A/Title: Molecular cloning of a gene expressed during early embryonic development in On  
A/Reference number: Z22341; MUID:95287898; PMID:7770081  
A/Accession: T43214  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-2022 <TRI>  
A/Cross-references: UNIPROT:P21249; EMBL:U12681; NID:G530824; PID:G530825; PIDD:AAA80005  
A/Experimental source: SPECIFIC host Homo sapiens  
R/Erondy, N.E.; Donelson, J.E.  
Mol. Biochem. Parasitol. 40, 213-224, 1990  
A/Title: Characterization of a myosin-like antigen from Onchocerca volvulus.

A/Reference number: A44939; MUID:90301142; PMID:2194123  
A/Accession: A44939  
A/Molecule type: mRNA  
A/Residues: 733-874 'E', 876-916 'S', 918-1038, 1040-1047, 'S', 1049-1283, 'E', 1285-1363 <ERO>  
A/Cross-references: GB:M30398  
A/Note: the sequence is revised in GenBank entry ONGANTMW, release 115. (PIDD:AAA29413.1)  
R/Donelson, J.E.; Duke, B.O.L.; Moser, D.; Zeng, W.; Erondy, N.E.; Lucius, R.; Renz, A.;  
Mol. Biochem. Parasitol. 31, 241-250, 1988  
A/Title: Construction of Onchocerca volvulus cDNA libraries and partial characterization  
A/Reference number: A54513; MUID:89127417; PMID:2464764  
A/Accession: A54513  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 733-866 <DON>  
A/Cross-references: GB:U03995; NID:g159874; PIDD:AAA29412.1; PID:g159875  
R/Nozi, E.; Erondy, N.E.; Donelson, J.E.  
submitted to the EMBL Data Library, April 1990  
A/Description: Characterization of a myosin-like antigen from Onchocerca volvulus.  
A/Reference number: S27825  
A/Accession: S27825  
A/Molecule type: mRNA  
A/Residues: 733-874 'E', 876-916 'S', 918-1038, 1040-1047, 'S', 1049-1283, 'E', 1285-1347, 'E', 1.  
A/Cross-references: EMBL:M30398; NID:g159876; PIDD:AAA29413.1; PID:g159877  
C/Genetics:  
A/Gene: ovtl  
C/Keywords: leucine zipper

Query Match 61.3%; Score 38; DB 2; Length 2022;  
Best Local Similarity 72.7%; Pred. No. 1.5e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IEALPRTHEQ 12  
:|:|:|:|:  
Db 292 IEAVKRFHEQ 302

RESULT 11  
D83156  
molybdopterin biosynthetic protein C PA3918 [imported] - Pseudomonas aeruginosa (strain I  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 16-Aug-2004  
C/Accession: D83156  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: D83156  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-160 <STO>  
A/Cross-references: UNIPROT:Q9HX95; GB:AE004809; GB:AE004091; NID:g9950097; PIDD:AA07300  
C/Genetics:  
A/Gene: moaC; PA3918  
A/Experimental source: strain PA01  
C/Superfamily: Molybdenum cofactor precursor 2 biosynthesis protein MoaC

Query Match 59.7%; Score 37; DB 2; Length 160;  
Best Local Similarity 70.0%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GIEALPRTHE 10  
:|:|:|:|:  
Db 60 GIQAKRTHE 69

RESULT 12  
H81834  
hypothetical protein NMA1441 [imported] - Neisseria meningitidis (strain Z2491 serogroup  
C/Species: Neisseria meningitidis  
C/Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C/Accession: H81834

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, H.; Holtz, S.; Jorgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: H81834  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-264 <PAR>  
A:Cross-references: UNIPROT:Q9JU90; GB:AL162756; GB:AL157959; NID:G7380091; PIDN:CA88467  
A:Experimental source: serogroup A, strain 22491  
C:Genetics:  
A:Gene: NMA1441  
C:Superfamily: *Neisseria meningitidis* hypothetical protein NMA1045

Query Match 59.7%; Score 37; DB 2; Length 264;  
Best Local Similarity 50.0%; Pred. No. 25;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTHESQ 12  
DB 134 GLEAIARVHKQ 145

RESULT 13  
AF2962  
A:Title: The genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AF2962  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-450 <KUR>  
A:Cross-references: UNIPROT:Q8UAS0; GB:AE008689; PIDN:AL14116.1; PID:G17741685; GSPDB:C  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu3300  
A:Map position: linear chromosome  
C:Superfamily: beta-alanine-pyruvate transaminase

Query Match 58.1%; Score 36; DB 2; Length 450;  
Best Local Similarity 70.0%; Pred. No. 69;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEALPRTHES 11  
DB 161 ITGLPRNHS 170

RESULT 14  
H98320  
A:Title: The genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* (strain C58).  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: H98320  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-450 <KUR>

A:Cross-references: UNIPROT:Q8UAS0; GB:AE007870; PIDN:AAK90090.1; PID:G15160077; GSPDB:C  
A:Genetics:  
A:Gene: AGR\_L\_3037  
A:Map position: linear chromosome  
C:Superfamily: beta-alanine-pyruvate transaminase

Query Match 58.1%; Score 36; DB 2; Length 450;  
Best Local Similarity 70.0%; Pred. No. 69;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEALPRTHES 11  
DB 161 ITGLPRNHS 170

RESULT 15  
S52469  
SOX9 protein - mouse  
C:Species: *Mus musculus* (house mouse)  
C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 16-Aug-2004  
C:Accession: S52469  
R:Wright, E.; Hargrave, M.R.; Christensen, J.; Cooper, L.; Kun, J.; Evans, T.; Gangadha  
Nature Genet. 9, 15-20, 1995  
A:Title: The *Sry*-related gene *Sox9* is expressed during chondrogenesis in mouse embryos.  
A:Reference number: S52469; MUID:95218811; PMID:7704017  
A:Accession: S52469  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-507 <WRI>  
A:Cross-references: UNIPROT:Q04887  
C:Superfamily: HMG box homology  
P:102-177/Domain: HMG box homology <HMG1>

Query Match 58.1%; Score 36; DB 2; Length 507;  
Best Local Similarity 41.7%; Pred. No. 78;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTHESQ 12  
DB 483 GVPSIPQTHSPQ 494

RESULT 16  
A55204  
transcription factor SOX9 - human  
N:Alternate names: sex-determining region Y box 9 protein  
C:Species: *Homo sapiens* (man)  
C:Date: 27-Jan-1995 #sequence\_revision 31-Dec-1995 #text\_change 09-Jul-2004  
C:Accession: A55204; S50851; S57725  
R:Wagner, T.; Birch, J.; Meyer, J.; Zabel, B.; Held, M.; Zimmer, J.; Brice  
Cell 79, 1111-1120, 1994  
A:Title: Autosomal sex reversal and campomelic dysplasia are caused by mutations in and  
A:Reference number: A55204; MUID:95094274; PMID:8001137  
A:Accession: A55204  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-509 <WAG>  
A:Cross-references: UNIPROT:P48436; GB:S74506; NID:9807059; PIDN:AA32870.1; PID:9807060  
R:Foster, J.W.; Dominguez-Steglich, M.A.; Gujoll, S.; Kwok, C.; Weller, P.A.; Stevanovic  
Nature 372, 525-530, 1994  
A:Title: Campomelic dysplasia and autosomal sex reversal caused by mutations in an *SRY*-r  
A:Reference number: S50851; MUID:95082803; PMID:7990924  
A:Accession: S50851  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-509 <FOS>  
A:Cross-references: EMBL:Z46629; NID:G758102; PIDN:CA86598.1; PID:G758103  
C:Genetics:  
A:Gene: GDB:SOX9  
A:Cross-references: GDB:134730; OMIM:211970  
A:Map position: 17q24.3-17q25.1  
C:Superfamily: unassigned HMG box proteins; HMG box homology  
P:102-177/Domain: HMG box homology <HMG1>

Query Match 58.1%; Score 36; DB 2; Length 509;  
Best Local Similarity 41.7%; Pred. No. 78;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GIEALPRTHEQ 12  
|: : : : :|  
Db 485 GVPSPQTHSPQ 496

## RESULT 17

polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) alpha chain [similarity] - Strept  
N:Alternate names: guanosine pentaphosphate synthetase [misidentification]  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: T10932; T35837  
R:Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, August 1998  
A:Reference number: Z17215  
A:Accession: T10932  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-716 <PAR>  
A:Cross-references: UNIPROT:Q8CJQ6; EMBL:AL031231; NID:G3413388; PIDN:CAA20272.1; PID:G3  
A:Experimental source: strain A3(2)  
R:Hariri, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, August 1998  
A:Reference number: Z21590  
A:Accession: T35837  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 683-739 <HAR>  
A:Cross-references: EMBL:AL031260; NID:G3413819; PIDN:CAA20288.1; PID:G3413820; GSPDB:GN  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: gptI; SCOEDB:SC9A10.01  
C:Superfamily: polyribonucleotide nucleotidyltransferase  
C:Keywords: nucleotidyltransferase

Query Match 58.1%; Score 36; DB 2; Length 739;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 IEALPRTHE 11  
|: : : : :|  
Db 355 VEAIPRVHGS 364

## RESULT 18

conserved hypothetical protein VC0429 [imported] - Vibrio cholerae (strain N16961 sero  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: D82324  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamthekhan, J.; Bass, S.; Qin, H.; Dragot, I.; Sellers, F  
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: D82324  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <HEI>  
A:Cross-references: UNIPROT:Q9KUT6; GB:AE004130; GB:AE003852; NID:G9654845; PIDN:AAF9360  
C:Genetics:  
A:Experimental source: serogroup O1, strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC0429  
A:Map position: 1

Query Match 58.1%; Score 36; DB 2; Length 854;  
Best Local Similarity 54.5%; Pred. No. 1.4e+02;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GIEALPRTHE 11  
|: : : : :|  
Db 345 GMSGLPRRHQS 355

## RESULT 19

vanillin dehydrogenase [imported] - Caulobacter crescentus  
A:87547  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: A87547  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolome  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: A87547  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-470 <STO>  
A:Cross-references: UNIPROT:Q9A5P5; GB:AE005673; NID:G13423939; PIDN:AAK24373.1; GSPDB:GT  
C:Genetics:  
A:Gene: CC2402  
C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 56.5%; Score 35; DB 2; Length 470;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 EALPRTHE 10  
|: : : : :|  
Db 163 ESCRTRHE 170

## RESULT 20

phosphoprotein phosphatase (EC 3.1.3.16) ppt-1 [similarity] - Neurospora crassa  
T46576  
N:Alternate names: serine/threonine phosphatase PPS homolog  
C:Species: Neurospora crassa  
C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 28-Apr-2003  
C:Accession: T46576  
R:Yatzen, E.; Yarden, O.  
submitted to the EMBL Data Library, February 1997  
A:Description: Ppt-1, a N. crassa novel-type phosphatase.  
A:Reference number: Z23089  
A:Accession: T46576  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-479 <YAT>  
A:Cross-references: EMBL:U89985; PIDN:AA65138.1  
C:Genetics:  
A:Gene: ppt-1  
A:Map position: V  
C:Superfamily: protein phosphatase 5; phosphoserine core homology; phosphoprotein phos  
C:Keywords: iron; metalloprotein; nucleus; phosphoric monoester hydrolase; zinc  
F:8-41/Domain: tetratricopeptide repeat homology <TT1>  
F:42-75/Domain: tetratricopeptide repeat homology <TT3>  
F:76-109/Domain: tetratricopeptide repeat homology <TT3>  
F:183-448/Domain: phosphoprotein phosphatase homology <PPP>  
F:215-284/Domain: phosphoserine core homology <PPC>  
F:221-223/Binding site: iron (Asp, His, Asp) #status predicted  
F:250-282,331,408/Binding site: zinc (Asp, Asn, His, His) #status predicted  
F:253,283,432/Active site: Asp, His, Tyr #status predicted  
F:254,381/Binding site: substrate phosphate (Arg) #status predicted

Query Match 56.5%; Score 35; DB 1; Length 479;  
Best Local Similarity 60.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GIEALPRTHE 10

Db 400 GLEAIRSHE 409

## RESULT 21

T12094  
beta-fructofuranosidase (EC 3.2.1.26) - fava bean  
C:Species: Vicia faba (fava bean)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T12094  
R:Weber, H.; Borstjuk, L.; Heim, U.; Buchner, P.; Wobue, U.  
Plant Cell 7, 1835-1846, 1995  
A:Title: Seed coat-associated invertases of Fava bean control both unloading and storage  
A:Reference number: Z17416; MUID:96093423; PMID:8535137  
A:Accession: T12094  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-575 <WEB>  
A:Cross-references: UNIPROT:Q43855; EMBL:Z35162; NID:g861154; PIDN:CAA84526.1; PID:g8611  
A:Experimental source: cv. Frifo, seed coat  
C:Genetics:  
A:Gene: CMINV1  
C:Superfamily: beta-fructofuranosidase  
C:Keywords: cell wall, glycoprotein, glycosidase, hydrolase

Query Match 56.5%; Score 35; DB 2; Length 575;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLEALPRT 8  
Db 350 GLEALPRT 357

## RESULT 22

T01575  
beta-fructofuranosidase (EC 3.2.1.26) INCW2 - maize  
N:Alternate names: invertase  
C:Species: Zea mays (maize)  
C:Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 09-Jul-2004  
R:Taliercio, E.; Chourey, P.; Shanker, S.; Choi, J.  
submitted to the EMBL Data Library, February 1998  
A:Reference number: Z14354  
A:Accession: T01575  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-593 <TAL>  
A:Cross-references: UNIPROT:O81189; EMBL:AF050631; NID:g3372517; PIDN:MAC28320.1; PID:g3  
A:Experimental source: tissue type kernel  
C:Genetics:  
A:Note: INCW2  
C:Function:  
A:Description: catalyzes hydrolysis of terminal non-reducing beta-D-fructofuranoside  
C:Superfamily: beta-fructofuranosidase  
C:Keywords: glycosidase; hydrolase

Query Match 56.5%; Score 35; DB 2; Length 593;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLEALPRT 8  
Db 362 GLEALPRT 369

## RESULT 23

S76615  
hypothetical protein - Synecchocystis sp. (strain PCC 6803)  
C:Species: Synecchocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S76615

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis  
sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S76615  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-603 <KAN>  
A:Cross-references: UNIPROT:Q55806; EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BAI1055  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Superfamily: threonine-tRNA ligase

Query Match 56.5%; Score 35; DB 2; Length 603;  
Best Local Similarity 77.8%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ALPRTSESQ 12  
Db 12 ALPRTSESQ 20

## RESULT 24

T24486  
hypothetical protein T05A1.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T24486  
R:Lloyd, C.  
submitted to the EMBL Data Library, December 1995  
A:Reference number: Z19897  
A:Accession: T24486  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-683 <WIL>  
A:Cross-references: UNIPROT:Q22187; EMBL:Z68219; PIDN:CAA92480.1; GSPDB:GN00022; CESP:TO  
A:Experimental source: clone T05A1  
C:Genetics:  
A:Gene: CESP:T05A1.3  
A:Map position: 4  
A:Introns: 54/3; 115/3; 165/2; 207/2; 293/2; 336/3; 375/3; 411/3; 448/3; 473/3; 531/3; 6

Query Match 56.5%; Score 35; DB 2; Length 683;  
Best Local Similarity 70.0%; Pred. No. 1.7e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LEALPRTSES 11  
Db 551 LEALPRTSES 560

## RESULT 25

B97123  
polyribonucleotide nucleotidyltransferase [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: B97123  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, O.; Gibson, R.; Lee,  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: B97123  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-703 <KUR>  
A:Cross-references: UNIPROT:O97145; GB:AB001437; PIDN:AAK79773.1; PID:g15024781; GSPDB:G  
A:Experimental source: Clostridium acetobutylicum ATCC624  
C:Genetics:  
A:Gene: CAC1808  
C:Superfamily: polyribonucleotide nucleotidyltransferase

Query Match 56.5%; Score 35; DB 2; Length 703;  
Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Cy 2 IEALPRTTHS 11  
Db 328 VDLPLRTHGS 337

RESULT 26  
A71069  
hypothetical protein PH1246 - *Pyrococcus horikoshii*  
C/Species: *Pyrococcus horikoshii*  
C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
C/Accession: A71069  
R;Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekit  
M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A/Reference number: A71000; MUID:98344137; PMID:9679194  
A/Accession: A71069  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-727 <KAM>  
A/Cross-references: UNIPROT:O58935; GB:AP000005; NID:93236132; PIDN:BA30347.1; PID:d103  
A/Experimental source: strain OT3  
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C/Genetics:  
A/Gene: PH1246

Query Match 56.5%; Score 35; DB 2; Length 727;  
Best Local Similarity 60.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Cy 1 GIEALPRTHE 10  
Db 649 GIEALPRTYQ 658

RESULT 27  
H90607  
atp-dependent helicase pcrA [imported] - *Mycoplasma pulmonis* (strain UAB CTTP)  
C/Species: *Mycoplasma pulmonis*  
C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C/Accession: H90607  
R;Chambaud, I.; Heilly, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;  
Nucleic Acids Res. 29, 2145-2153, 2001  
A/Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulm*  
A/Reference number: A99512; MUID:21267165; PMID:11353084  
A/Accession: H90607  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-741 <KTR>  
A/Cross-references: UNIPROT:Q99PF5; GB:A1445566; PID:g14090183; PIDN:CAC13941.1; GSPDB:C  
A/Experimental source: strain UAB CTTP  
C/Genetics:  
A/Gene: MYPV 7680  
C/Superfamily: SGC3  
A/Superfamily: helicase II

Query Match 56.5%; Score 35; DB 2; Length 741;  
Best Local Similarity 54.5%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 GIEALPRTTHS 11  
Db 725 GIRTISTKTHS 735

RESULT 28  
D84595  
PEAR1 4 protein [imported] - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: D84595  
R;Lin, X.; Kall, S.; Rounsley, S.D.; Shea, T.P.; Benteo, M.I.; Town, C.D.; Fujii, C.Y.; M;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: D84595  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-748 <STO>  
A/Cross-references: UNIPROT:Q95KR5; GB:AE002093; NID:g4803947; PIDN:AAD29820.1; GSPDB:GNK  
C/Genetics:  
A/Gene: At2g20960  
A/Map position: 2

Query Match 56.5%; Score 35; DB 2; Length 748;  
Best Local Similarity 54.5%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 2 IEALPRTTHSQ 12  
Db 380 VETKPRTHESR 390

RESULT 29  
D64902  
hypothetical protein b1489 - *Escherichia coli* (strain K-12)  
C/Species: *Escherichia coli*  
C/Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 16-Aug-2004  
C/Accession: D64902  
R;Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coj  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A/Title: The complete genome sequence of *Escherichia coli* K-12.  
A/Reference number: A64720; MUID:97426617; PMID:9278503  
A/Accession: D64902  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-807 <BIAT>  
A/Cross-references: GB:AE000246; GB:U00096; NID:g1787764; PIDN:AACT4562.1; PID:g1787765;  
A/Experimental source: strain K-12, substrain MG1655  
C/Superfamily: Oxygen sensor diguanylate cyclase/c-di-GMP phosphodiesterase

Query Match 56.5%; Score 35; DB 2; Length 807;  
Best Local Similarity 70.0%; Pred. No. 2e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 1 GIEALPRTHE 10  
Db 582 GIEALRMD 591

RESULT 30  
AF1082  
B. subtilis yoka protein homolog lmo0061 [imported] - *Listeria monocytogenes* (strain EGD  
C/Species: *Listeria monocytogenes*  
C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C/Accession: AF1082  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Feihl, H.  
D.; Jones, L.M.; Karet, U.  
Science 294, 849-852, 2001  
A/Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurupkat, G.; Madueno, E.; Maicournam, A.; Ma  
ok, C.; Schluter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,  
A/Title: Comparative genomics of *Listeria species*.  
A/Reference number: AB1077; MUID:21537279; PMID:11679669  
A/Accession: AF1082  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1498 <GLA>  
A/Cross-references: UNIPROT:Q8YA05; GB:NC\_003210; PIDN:CAC98276.1; PID:g16409420; GSPDB:

A;Experimental source: strain EGD-e  
C;Genetics:  
A;Gene: lmc0061

Query Match 56.5%; Score 35; DB 2; Length 1498;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIEALPR 7  
|||  
Db 941 GIEALPR 947

Search completed: August 1, 2005, 08:49:02  
Job time : 44 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: August 1, 2005, 08:26:18 ; Search time 173 Seconds  
(without alignments)  
35.520 Million cell updates/sec

Title: US-10-663-749-18  
Perfect score: 62  
Sequence: 1 GIBALPRTMSQ 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	500	1 PRC1_HUMAN	Q16647 homo sapien
2	62	100.0	500	2 Q6LBN2	Q6LBN2 homo sapien
3	62	100.0	509	2 Q6LBN0	Q6LBN0 homo sapien
4	55	88.7	168	2 Q7TSX2	Q7TSX2 mus musculu
5	55	88.7	501	1 PRC1_MOUSE	Q35074 mus musculu
6	55	88.7	501	1 PRC1_RAT	Q62969 rattus norv
7	55	88.7	509	2 Q6BXC0	Q6BXC0 mus musculu
8	43	69.4	1534	2 Q7QTR2	Q7QTR2 giardia lam
9	42	67.7	310	2 Q6MLK6	Q6MLK6 bdellovibri
10	41	66.1	134	2 Q6S5C7	Q6S5C7 capra hircu
11	41	66.1	500	1 PRC1_BOVIN	Q29626 bos taurus
12	41	66.1	802	2 Q87L51	Q87L51 vibrio para
13	41	66.1	399	2 Q92M18	Q92M18 rhizobium m
14	40	64.5	880	2 Q9SVU3	Q9SVU3 arabidopsis
15	40	64.5	924	2 Q949M4	Q949M4 arabidopsis
16	40	64.5	2530	2 Q6RKG3	Q6RKG3 mycoplasmae
17	39	62.9	248	2 Q87XK6	Q87XK6 pseudomonas
18	39	62.9	271	2 Q9V4P7	Q9V4P7 drosophila
19	39	62.9	283	2 Q87Q39	Q87Q39 vibrio para
20	39	62.9	294	2 Q6CKA0	Q6CKA0 kluyveromyc
21	39	62.9	310	2 Q7JY81	Q7JY81 mycobacteri
22	39	62.9	364	2 Q6A8K2	Q6A8K2 propionibac
23	39	62.9	367	2 Q8XA08	Q8XA08 escherichia
24	39	62.9	400	2 Q86L11	Q86L11 dictyosteli
25	39	62.9	838	2 Q9HC82	Q9HC82 homo sapien
26	39	62.9	1001	2 Q6AHZ6	Q6AHZ6 homo sapien
27	39	62.9	1001	2 Q7L3T6	Q7L3T6 homo sapien
28	39	62.9	1030	2 Q7S150	Q7S150 homo sapien
29	38	61.3	127	2 Q7YUM6	Q7YUM6 trypanosoma
30	38	61.3	310	2 Q8C1T4	Q8C1T4 mus musculu
31	38	61.3	350	2 Q923H4	Q923H4 mus musculu

32	38	61.3	442	2 Q9R214	Q9R214 deinococcus
33	38	61.3	475	2 Q96FB5	Q96FB5 homo sapien
34	38	61.3	475	2 Q9Y358	Q9Y358 homo sapien
35	38	61.3	475	2 Q6AYC0	Q6AYC0 rattus norv
36	38	61.3	475	2 Q8BZG5	Q8BZG5 mus musculu
37	38	61.3	599	2 Q88U93	Q88U93 lactobacilli
38	38	61.3	765	2 Q729M0	Q729M0 trichoderma
39	38	61.3	869	2 Q65ZC5	Q65ZC5 caenorhabdi
40	38	61.3	937	1 YM92_CABEL	YM92_CABEL
41	38	61.3	1312	2 Q8W272	Q8W272 caenorhabdi
42	38	61.3	2022	1 ANT1_ONCVO	ANT1_ONCVO
43	37	59.7	160	1 MOAC_PSEAE	MOAC_PSEAE
44	37	59.7	203	2 Q73UH7	Q73UH7 mycobacteri
45	37	59.7	242	2 Q83GA6	Q83GA6 tropheryma
46	37	59.7	242	2 Q83NM0	Q83NM0 tropheryma
47	37	59.7	264	2 Q9J090	Q9J090 neisseria m
48	37	59.7	284	2 Q7QDZ7	Q7QDZ7 anopheles g
49	37	59.7	307	1 BBP2_DROME	BBP2_DROME
50	37	59.7	346	2 Q7PKV2	Q7PKV2 anopheles g
51	37	59.7	462	2 Q72AB3	Q72AB3 desulfovibr
52	37	59.7	672	2 Q25586	Q25586 onchocerca
53	37	59.7	736	2 Q6EB02	Q6EB02 reovirus ty
54	37	59.7	801	2 Q6LVH4	Q6LVH4 photobacter
55	37	59.7	978	1 LIDS_GABGR	LIDS_GABGR
56	37	59.7	978	1 Q81LS2	Q81LS2 plasmodium
57	37	59.7	136	2 Q8N589	Q8N589 homo sapien
58	37	59.7	146	2 Q8J228	Q8J228 aspergillus
59	36	58.1	151	2 Q7M7A4	Q7M7A4 photorhabd
60	36	58.1	164	2 Q8FDM0	Q8FDM0 escherichia
61	36	58.1	179	2 Q74MM9	Q74MM9 nanarchaeu
62	36	58.1	185	2 Q7RPU7	Q7RPU7 plasmodium
63	36	58.1	193	1 GRPE_BACTN	GRPE_BACTN
64	36	58.1	233	2 Q7UR56	Q7UR56 rhodospirall
65	36	58.1	234	2 Q9F8X4	Q9F8X4 pseudomonas
66	36	58.1	240	2 Q8XUS6	Q8XUS6 talstonia s
67	36	58.1	265	2 Q91B78	Q91B78 rana rugosa
68	36	58.1	320	2 Q9VZW4	Q9VZW4 drosophila
69	36	58.1	333	2 Q67P85	Q67P85 symbiodacte
70	36	58.1	397	2 Q7X7E2	Q7X7E2 oryza sativ
71	36	58.1	450	2 Q8UAS0	Q8UAS0 agrobacteri
72	36	58.1	476	2 Q6DFP5	Q6DFP5 xenopus lae
73	36	58.1	477	2 Q90YL1	Q90YL1 xenopus lae
74	36	58.1	482	2 Q76K22	Q76K22 streptococc
75	36	58.1	482	2 Q6F2E7	Q6F2E7 xenopus tro
76	36	58.1	482	2 Q91B79	Q91B79 rana rugosa
77	36	58.1	490	2 Q9DBE8	Q9DBE8 eubiepharis
78	36	58.1	494	2 Q73668	Q73668 gallus gall
79	36	58.1	495	2 Q9YGP7	Q9YGP7 alligator m
80	36	58.1	507	1 SOX9_MOUSE	SOX9_MOUSE
81	36	58.1	509	1 SOX9_HUMAN	SOX9_HUMAN
82	36	58.1	509	1 SOX9_MACMU	SOX9_MACMU
83	36	58.1	509	1 SOX9_PANTR	SOX9_PANTR
84	36	58.1	509	1 SOX9_PIG	SOX9_PIG
85	36	58.1	509	1 SOX9_PONPY	SOX9_PONPY
86	36	58.1	509	2 Q9BG51	Q9BG51 callichris
87	36	58.1	509	2 Q9BG92	Q9BG92 hylobates s
88	36	58.1	511	2 Q6N6F2	Q6N6F2 rhodospendo
89	36	58.1	513	2 Q7YR07	Q7YR07 canis famli
90	36	58.1	531	2 Q6DD25	Q6DD25 xenopus lae
91	36	58.1	540	1 HCP_METMA	HCP_METMA
92	36	58.1	546	2 Q8DWZ1	Q8DWZ1 streptococc
93	36	58.1	546	2 Q8E2U2	Q8E2U2 streptococc
94	36	58.1	571	2 Q7OF13	Q7OF13 anopheles g
95	36	58.1	640	2 Q6FJ14	Q6FJ14 candida gla
96	36	58.1	656	2 Q7Q036	Q7Q036 oryza sativ
97	36	58.1	671	2 Q7XHY3	Q7XHY3 anopheles g
98	36	58.1	679	2 Q86OH5	Q86OH5 anopheles g
99	36	58.1	687	2 Q9NKV3	Q9NKV3 bombyx mori
100	36	58.1	738	2 Q82K80	Q82K80 streptomyce
101	36	58.1	749	2 Q8CJ06	Q8CJ06 streptomyce
102	36	58.1	739	2 Q53597	Q53597 streptomyce
103	36	58.1	854	2 Q9KUT6	Q9KUT6 vibrio chol
104	36	58.1	859	2 Q9UIR3	Q9UIR3 caenorhabdi

105	36	58.1	892	2	Q89G03	Q89G03 bradyrhizob
106	36	58.1	933	2	Q7SFQ3	Q7SFQ3 neurospora
107	36	58.1	940	2	Q9RDJ6	Q9RDJ6 streptomyces
108	36	58.1	1004	2	Q7RBD2	Q7RBD2 plasmidum
109	36	58.1	1114	2	Q6VQA2	Q6VQA2 brachydanio
110	36	58.1	1134	2	Q8G8R4	Q8G8R4 streptomyces
111	36	58.1	1340	2	Q9VPR5	Q9VPR5 drosophila
112	36	58.1	1805	1	RW1_HUMAN	Q92545 homo sapien
113	36	56.5	89	2	Q93J17	Q93J17 streptomyces
114	36	56.5	168	2	Q63V56	Q63V56 burkholderi
115	36	56.5	192	2	Q17211	Q17211 bombyx mori
116	36	56.5	200	2	Q63T81	Q63T81 burkholderi
117	36	56.5	230	2	Q8L2F0	Q8L2F0 acoeloplathu
118	36	56.5	234	1	ISPDI3	Q8L191 synecococc
119	36	56.5	246	2	Q7P1J3	Q7P1J3 chromobacte
120	36	56.5	264	2	Q89QM7	Q89QM7 bradyrhizob
121	36	56.5	284	2	Q8XZQ4	Q8XZQ4 ralscristia s
122	36	56.5	293	2	Q8E1J6	Q8E1J6 shewanella
123	36	56.5	306	2	Q8BL96	Q8BL96 mus musculu
124	36	56.5	318	2	Q87KY9	Q87KY9 vibrio para
125	36	56.5	349	2	Q6ZN99	Q6ZN99 homo sapien
126	36	56.5	349	2	Q7S3D8	Q7S3D8 neurospora
127	36	56.5	373	2	Q8QLT3	Q8QLT3 mamestra co
128	36	56.5	373	2	Q7IAG1	Q7IAG1 mamestra co
129	36	56.5	404	2	Q7SIW0	Q7SIW0 neurospora
130	36	56.5	424	2	Q6ZHU5	Q6ZHU5 burkholderi
131	36	56.5	424	2	Q63WK4	Q63WK4 burkholderi
132	36	56.5	426	2	Q6MN74	Q6MN74 belliovibri
133	36	56.5	436	2	Q9PUJ5	Q9PUJ5 carassius a
134	36	56.5	456	2	Q86LH6	Q86LH6 venturia ca
135	36	56.5	470	2	Q9A5P5	Q9A5P5 caulobacter
136	36	56.5	479	2	Q144Z8	Q144Z8 neurospora
137	36	56.5	479	2	Q6B7J1	Q6B7J1 epinephelus
138	36	56.5	482	2	Q90Z23	Q90Z23 monopterus
139	36	56.5	484	2	Q8UWL6	Q8UWL6 figu rubrip
140	36	56.5	494	1	Q9DE39	Q9DE39 oncothyridu
141	36	56.5	494	1	SOX9_CHICK	Q48434 gallus galli
142	36	56.5	498	2	Q8K4P9	Q8K4P9 mus musculu
143	36	56.5	505	2	Q7XVW4	Q7XVW4 oryza sativ
144	36	56.5	517	2	Q7RM94	Q7RM94 neurospora
145	36	56.5	531	2	Q6FV66	Q6FV66 candida gla
146	36	56.5	541	2	Q6PCP6	Q6PCP6 mus musculu
147	36	56.5	550	2	Q73RPS	Q73RPS treponema d
148	36	56.5	550	1	Q73RPS	Q73RPS homo sapien
149	36	56.5	555	1	SYT8_HUMAN	Q7RN84 mus musculu
150	36	56.5	575	2	Q43855	Q43855 vicia faba

## ALIGNMENTS

RESULT 1  
PTGI\_HUMAN STANDARD; PRT; 500 AA.  
AC Q16647; Q9HAX2; Q9HAX3; Q9HAX4;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Prostacyclin synthase (EC 5.3.99.4) (Prostaglandin I2 synthase).  
GN Name=PTGIS; Synonyms=CYP8, CYP8A1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Aorta;  
RX MEDLINE=9424046; PubMed=8185632;  
RA Miyata A., Hara S., Yokoyama C., Inoue H., Ullrich V., Tanabe T.;  
RT "Molecular cloning and expression of human prostacyclin synthase";  
RL Biochem. Biophys. Res. Commun. 200:1728-1734(1994).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANTS LEU-38; ARG-118 AND SER-379.

CC MEDLINE=21177061; PubMed=11281454;  
CC RA Chevalier D., Cauffiez C., Bernard C., Lo-Guidice J.-M., Allorge D.,  
CC RA Fazio F., Ferrari N., Liberra C., Lhermitte M., D'Halluin J.C.,  
CC RA Broly F.;  
CC "Characterization of new mutations in the coding sequence and 5'-  
CC untranslated region of the human prostacyclin synthase gene  
CC (CYP8A1).";  
CC Hum. Genet. 108:148-155(2001).  
CC [3]  
CC RP SEQUENCE FROM N.A.  
CC RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
CC RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
CC RA Jones M., Stavrides G., Almeida J.P., Babage A.K., Baguley C.L.,  
CC RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
CC RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
CC RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
CC RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
CC RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
CC RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
CC RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
CC RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
CC RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
CC RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
CC RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
CC RA Leharasliho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
CC RA Marsh V.L., Martin S.L., McConachie L.J., McHay K., McMurtry A.A.,  
CC RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
CC RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
CC RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramay H.,  
CC RA Rice C.M., Ross M.T., Scott C.E., Senra H.K., Showgreen R., Sims S.,  
CC RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
CC RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
CC RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
CC RA Whitehead S.L., Whitteker P., Willey D.L., Williams L., Williams S.A.,  
CC RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
CC RA Rogers J.;  
CC "The DNA sequence and comparative analysis of human chromosome 20.";  
CC Nature 414:865-871(2001).  
CC RL -1- FUNCTION: Catalyzes the isomerization of prostaglandin H2 to  
CC prostacyclin (= prostaglandin I2).  
CC CC -1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9- $\alpha$ -11- $\alpha$ -epidixy-15-  
CC hydroxyprosta-5,13-dienoate = (5Z,13E)-(15S)-6,9- $\alpha$ -epoxy-11-  
CC  $\alpha$ -15-dihydroxyprosta-5,13-dienoate.  
CC CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane. May be  
CC anchored to the membrane via a single transmembrane domain.  
CC CC -1- TISSUE SPECIFICITY: Widely expressed; particularly abundant in  
CC ovary, heart, skeletal muscle, lung and prostate.  
CC CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
CC CC -1- DATABASE: NMB=Cytochrome P450 Allele Nomenclature Committee;  
CC NOTE=CYP8A1 alleles;  
CC WWW="http://www.jim.ki.se/cypalleles/cyp8a1.htm".  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
CC EMBL; D38145; BAA07343.1; -;  
CC EMBL; AF297048; AAG31781.1; -;  
CC EMBL; AF297049; AAG31782.1; -;  
CC EMBL; AF297050; AAG31783.1; -;  
CC EMBL; AF297051; AAG31784.1; -;  
CC EMBL; AF297052; AAG31785.1; -;  
CC EMBL; AL118525; CAC14162.1; -;  
CC PIR; JC2231; JC2231.1; -;  
CC Gene; HGNC:9603; PTGIS.  
CC MIM; 601699; -;  
CC GO; GO:0008116; P:prostaglandin-I synthase activity; TAS.  
CC InterPro; IPR001128; Cytochrome\_P450.  
CC InterPro; IPR002403; EP4501V.

```
DR Pfam: PF00067; P450; 2.
DR PRINTS; PRO0465; EP450IV.
DR PRINTS; PRO0385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.
KW Endoplasmic reticulum; Heme; Isomerase; Polymorphism;
KW Prostaglandin biosynthesis; Transmembrane.
FT TRANSMEM 1 20
FT METAL 441 441
FT VARIANT 38 38
FT VARIANT 118 118
FT VARIANT 154 154
FT VARIANT 171 171
FT VARIANT 236 236
FT VARIANT 379 379
FT VARIANT 500 500
SQ SEQUENCE 500 AA; 57103 MW; 39595442BFC0B625 CRC64;
Query Match 100.0%; Score 62; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GIEALPRTHEQ 12
Db 182 GIEALPRTHEQ 193

RESULT 2
QLEND2 PRELIMINARY; PRT; 500 AA.
ID QLEND2
AC 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Prostacyclin synthase (EC 5.3.99.4).
GN Name:PTGIS(CYP8);
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94242046; PubMed=8185632;
RA Miyata A., Hara S., Yokoyama C., Inoue H., Ullrich V., Tanabe T.;
RT "Molecular cloning and expression of human prostacyclin synthase.";
RL Biochem. Biophys. Res. Commun. 200:1728-1734(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96411687; PubMed=8812456; DOI=10.1006/geno.1996.0465;
RA Yokoyama C., Yabuki T., Inoue H., Tone Y., Hara S., Hatae T.,
RA Nagata M., Takahashi E.-I., Tanabe T.;
RT "Human gene encoding prostacyclin synthase (PTGIS): genomic
RT organization, chromosomal localization, and promoter activity.";
RL Genomics 36:296-304(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Tanabe T.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; D83393; BAA11910.1; JOINED.
DR EMBL; D83394; BAA11910.1; JOINED.
DR EMBL; D83395; BAA11910.1; JOINED.
DR EMBL; D83396; BAA11910.1; JOINED.
DR EMBL; D83397; BAA11910.1; JOINED.
DR EMBL; D83398; BAA11910.1; JOINED.
DR EMBL; D83399; BAA11910.1; JOINED.
DR EMBL; D83400; BAA11910.1; JOINED.
```

```
DR EMBL; D83401; BAA11910.1; JOINED.
DR EMBL; D83402; BAA11910.1; -.
DR GO; GO:0016953; F:isomerase activity; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0008116; F:prostaglandin-I synthase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002403; EP450IV.
DR PRINTS; PRO0465; EP450IV.
DR PRINTS; PRO0385; P450.
KW Cyclin; Heme; Isomerase.
SQ SEQUENCE 500 AA; 57131 MW; 9DC13CF771C3BED CRC64;
Query Match 100.0%; Score 62; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GIEALPRTHEQ 12
Db 191 GIEALPRTHEQ 202

RESULT 3
QLEND0 PRELIMINARY; PRT; 509 AA.
ID QLEND0
AC 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Prostacyclin synthase (EC 5.3.99.4) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Japanese; TISSUE=Leucocyte;
RX MEDLINE=96205357; PubMed=8630042; DOI=10.1006/dbrc.1996.0677;
RA Nakayama T., Soma M., Izumi Y., Kamatsuse K.;
RT "Organization of the human prostacyclin synthase gene.";
RL Biochem. Biophys. Res. Commun. 221:803-806(1996).
CC -1 SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; D84115; BAA28219.1; JOINED.
DR EMBL; D84116; BAA28219.1; JOINED.
DR EMBL; D84117; BAA28219.1; JOINED.
DR EMBL; D84118; BAA28219.1; JOINED.
DR EMBL; D84119; BAA28219.1; JOINED.
DR EMBL; D84120; BAA28219.1; JOINED.
DR EMBL; D84121; BAA28219.1; JOINED.
DR EMBL; D84122; BAA28219.1; JOINED.
DR EMBL; D84123; BAA28219.1; JOINED.
DR GO; GO:0016953; F:isomerase activity; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0008116; F:prostaglandin-I synthase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002403; EP450IV.
DR PRINTS; PRO0465; EP450IV.
DR PRINTS; PRO0385; P450.
KW Cyclin; Heme; Isomerase.
FT NON_TER 1
SQ SEQUENCE 509 AA; 57869 MW; 200FF90BFF62BCE CRC64;
```

```

RESULT 4
Q7TSX2 PRELIMINARY; PRT; 168 AA.
ID Q7TSX2
AC Q7TSX2;
DT 01-OCT-2003 (TEMBLrel. 25. Created)
DT 01-OCT-2003 (TEMBLrel. 25. Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26. Last annotation update)
DE Prostacyclin synthase (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kunming;
RA Ding N.-Z., He C.-Q., Yang Z.-M.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Kunming;
RA Ding N.-Z., He C.-Q., Yang Z.-M.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Kunming;
RA Ding N.-Z., He C.-Q., Yang Z.-M.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclochrome P450 family.
DR EMBL; AY285779; AAB37445.1; -.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR Cyclic; Heme; Monooxygenase; Oxidoreductase.
FT NON_TER
FT TER
SQ SEQUENCE 168 AA; 18896 MW; 59E78F4BFE6690B CRC64;

Query March 88.7%; Score 55; DB 2; Length 168;
Best Local Similarity 83.3%; Pred. No. 0.024;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1EALPRTHEQ 12
Db 5 GVEASPRTHSEQ 16

RESULT 5
PTGI_MOUSE STANDARD; PRT; 501 AA.
ID PTGI_MOUSE
AC 035074;
DT 16-OCT-2001 (Rel. 40. Created)
DT 16-OCT-2001 (Rel. 40. Last sequence update)
DT 25-OCT-2004 (Rel. 45. Last annotation update)
DE Prostacyclin synthase (EC 5.3.99.4) (Prostaglandin H2 synthase).
GN Name=Ptgis; Synonym=Cyp8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Peritoneal macrophage;
RA MEDLINE=9734566; PubMed=202154; DOI=10.1016/S0014-5793(97)00516-4;
RA Kuwamoto S., Inoue H., Tone Y., Izumi Y., Tanabe T.;
RT "Inverse gene expression of prostacyclin and thromboxane synthases in
RT resident and activated peritoneal macrophages.";
RL FEBS Lett. 409:242-246(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Testis;
RA MEDLINE=22354683; PubMed=1246685; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Osato N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
RA Balderelli R., Hill D.P., Bule C., Hume D.A., Quakenbush J.,
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dregani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

```

```

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimond S., Gustincich S., Hirokawa N., Jackson J.U., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierzki R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagasima T., Numata K., Okido T., Pavan W.J., Perlee G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lmb;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huily S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhe D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Catalyzes the isomerization of prostaglandin H2 to
CC prostacyclin (= prostaglandin I2).
CC -1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9-alpha,11-alpha-epidioxo-15-
CC hydroxyprosta-5,13-dienoate = (5Z,13E)-(15S)-6,9-alpha-epoxy-11-
CC alpha,15-dihydroxyprosta-5,13-dienoate.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane. May be
CC anchored to the membrane via a single transmembrane domain.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announce/
CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; AB001607; BAC21717.1; -.
CC EMBL; AK076885; BAC36403.1; -.
CC EMBL; BC062151; AAH62151.1; -.
CC MGD; MGI:1097156; Ptgis8.
CC InterPro; IPR001128; Cytochrome_P450.
CC InterPro; IPR002403; BP450IV.
CC Pfam; PF00067; P450; 2.
CC PRINTS; PR00465; BP450IV.
CC PRINTS; PR00385; P450.
CC PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.

```

KW Endoplasmic reticulum; Heme; Isomerase; Prostaglandin biosynthesis;  
 KW Transmembrane. 1 21 Potential.  
 FT TRANSMEM 442 442 Iron (heme axial ligand) (By similarity).  
 SO SEQUENCE 501 AA; 57046 MW; F018F5D3A1B0EBB CRC64;  
 Query Match 88.7%; Score 55; DB 1; Length 501;  
 Best Local Similarity 83.3%; Pred. NO. 0.077;  
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 G1EALPRTHEQ 12  
 |||||  
 Db 183 GVEASPRTHSQ 194

RESULT 6  
 PTGI RAT STANDARD; PRT; 501 AA.  
 AC Q62969;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Prostaglandin synthase (EC 5.3.99.4) (Prostaglandin 12 synthase).  
 GN Name:Ptgls; Synonyms:CYP8;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RA Geraci M.W., Gao B., Shepherd D., Moore M., Vernon J., Miller Y.E.,  
 RA Voelkel N.F.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Catalyzes the isomerization of prostaglandin H2 to  
 CC prostaglandin (= prostaglandin I2) (By similarity).  
 CC -1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9- $\alpha$ -11- $\alpha$ -epidioxo-15-  
 CC hydroxyprosta-5,13-dienoate = (5Z,13E)-(15S)-6,9- $\alpha$ -epoxy-11-  
 CC  $\alpha$ ,15-dihydroxyprosta-5,13-dienoate.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane. May be  
 CC anchored to the membrane via a single transmembrane domain.  
 CC -1- SIMILARITY: Belongs to the cyclooxygenase P450 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, US3855; AAB02322.1; -.  
 CC DR RGD; 3438; Ptgls.  
 CC DR InterPro; IPR001128; Cyclooxygenase\_P450.  
 CC DR InterPro; IPR002403; EP501V.  
 CC DR Pfam; PF000677; P450; 2.  
 CC DR PRINTS; PR00465; EP4501V.  
 CC DR PRINTS; PR00385; P450.  
 CC DR PROSITE; PS00086; CYTOCHROME\_P450; FALSE NEG.  
 KW Endoplasmic reticulum; Heme; Isomerase; Prostaglandin biosynthesis;  
 KW Transmembrane. 1 21 Potential.  
 FT TRANSMEM 442 442 Iron (heme axial ligand) (By similarity).  
 SO SEQUENCE 501 AA; 57127 MW; D2D85ADF3C464863 CRC64;  
 Query Match 88.7%; Score 55; DB 1; Length 501;  
 Best Local Similarity 83.3%; Pred. NO. 0.077;  
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 7  
 ID QBXCO PRELIMINARY; PRT; 509 AA.  
 AC QBXCO;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched  
 DE library, clone:Cl0032H06 product:prostaglandin 12 (prostaglandin)  
 DE synthase, full insert sequence.  
 GN Name:Ptgls;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6J; TISSUE=Head;  
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX RIKEN PANTOM Consortium; PubMed=11217851; DOI=10.1038/35055500;  
 RA "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 RN [3]  
 SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6J; TISSUE=Head;  
 RC The PANTOM Consortium;  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 RA 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RN [4]  
 SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6J; TISSUE=Head;  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subfraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes."  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6J; TISSUE=Head;  
 RC MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;  
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Kitounai T., Tashiro H., Itoh M.,  
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwa K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multiplexed sequencer."  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6J; TISSUE=Head;  
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraishi T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yaenishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
DR EMBL: AK048059; BAC33227.1; -.  
DR MGD: MGI:1097156; Prgis.  
DR GO: GO:0005615; C:extracellular space; TAS.  
DR InterPro: IPR001128; Cytochrome\_P450.  
DR InterPro: IPR002403; EP450IV.  
DR Pfam: PF00067; P450\_2.  
DR PRINTS: PR00465; EP450IV.  
DR PRINTS: PR00385; P450.  
KM Cyclin; Heme.  
SQ SEQUENCE 509 AA; 57769 MW; 732B51E854E70002 CRC64;  
Query Match 88.7%; Score 55; DB 2; Length 509;  
Best Local Similarity 83.3%; Pred. No. 0.078;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GIEALPRTHEQ 12  
DB 183 GVEASPRTHEQ 194  
RESULT 8  
Q7QTR2 PRELIMINARY; PRT; 1534 AA.  
AC Q7QTR2;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DS GLE\_510\_27846\_23242.  
OS Giardia lamblia ATCC 50803.  
CC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
OC NCBI\_TaxID=184922;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WB C6;  
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
RA Olsen G.J., Sogin M.L.;  
RL "Draft sequence of the Giardia lamblia genome.";  
RL Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
CC Preliminary data.  
DR EMBL: AAC01000102; EAA38417.1; -.  
SQ SEQUENCE 1534 AA; 171028 MW; 41A7EB9C9CAC36CF CRC64;  
Query Match 69.4%; Score 43; DB 2; Length 1534;  
Best Local Similarity 72.7%; Pred. No. 54;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 IEALPRTHEQ 12  
DB 1300 IAAMPRTHEQ 1310  
RESULT 9  
Q6MLK6 PRELIMINARY; PRT; 310 AA.  
AC Q6MLK6;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical transmembrane protein yneE.  
OS Name=yneE; OrderedLocNames=Bd2002;  
GN Bdellovibrio bacteriovorus.  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;  
OC Bdellovibrionaceae; Bdellovibrrio.  
CX NCBI\_TaxID=959;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;  
RX PubMed=14752164; DOI=10.1126/science.1093027;

RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,  
RA Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,  
RA Sockett R.E., Schuster S.C.;  
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a  
RT genomic perspective.";  
RL Science 303:689-692(2004).  
DR EMBL: BX842651; CAE79851.1; -.  
DR InterPro: IPR007913; UPF0187.  
DR Pfam: PF05249; UPF0187; 1.  
KM Complete proteome.  
SQ SEQUENCE 310 AA; 35262 MW; C469E4820D2A2A38 CRC64;  
Query Match 67.7%; Score 42; DB 2; Length 310;  
Best Local Similarity 66.7%; Pred. No. 15;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GIEALPRTHEQ 12  
DB 295 GERALPRNHEQ 306  
RESULT 10  
Q865C7 PRELIMINARY; PRT; 134 AA.  
AC Q865C7;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Prostacyclin synthase (Fragment).  
OS Capra hircus (Goat).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Caprinae; Capra.  
CX NCBI\_TaxID=9925;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kawate N., Tsuji M., Tamada H., Inaba T., Sawada T.;  
RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AY221118; AAO65922.1; -.  
KM Cyclin.  
FT NON\_TER 1 1  
FT NON\_TER 134 134  
SQ SEQUENCE 134 AA; 15105 MW; F7FF03CACBDAD6C4 CRC64;  
Query Match 66.1%; Score 41; DB 2; Length 134;  
Best Local Similarity 66.7%; Pred. No. 9.4;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GIEALPRTHEQ 12  
DB 46 GVEAPPTHEQ 57  
RESULT 11  
PTGI\_BOVIN STANDARD; PRT; 500 AA.  
AC Q29626; Q28841;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Prostacyclin synthase (EC 5.3.99.4) (Prostaglandin 12 synthase).  
GN Name=PTGIS; Synonyms=CYP8;  
OS Bos taurus (Bovine).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
CX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
RC TISSUE=Aorta;  
RX MEDLINE=94327536; PubMed=8051072;  
RA Hara S., Miyata A., Yokoyama C., Inoue H., Brugger R., Lottepeich F.,  
RA Ullrich V., Tanabe T.;

RT "Isolation and molecular cloning of prostacyclin synthase from bovine  
 RT endothelial cells." J. Biol. Chem. 269:19897-19903 (1994).  
 RN (2)  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Aorta;  
 RX MEDLINE=94354863; PubMed=8974709;  
 RA Pereira B., Wu K.K., Wang L.H.;  
 RT "Molecular cloning and characterization of bovine prostacyclin  
 synthase." J.  
 RL Biochem. Biophys. Res. Commun. 203:59-66 (1994).  
 RP [3]  
 RP SEQUENCE OF 9-30 FROM N.A.  
 RC TISSUE=Aorta;  
 RX MEDLINE=94107296; PubMed=8280118;  
 RA Pereira B., Wu K.K., Wang L.H.;  
 RT "Bovine prostacyclin synthase: purification and isolation of partial  
 cDNA." J.  
 RL Biochem. Biophys. Res. Commun. 197:1041-1048 (1993).  
 CC -1- FUNCTION: Catalyzes the isomerization of prostaglandin H2 to  
 CC prostacyclin (= prostaglandin I2).  
 CC -1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9- $\alpha$ ,11- $\alpha$ -epidioxo-15-  
 CC hydroxyprosta-5,13-dienoate = (5Z,13E)-(15S)-6,9- $\alpha$ -epoxy-11-  
 CC  $\alpha$ ,15-dihydroxyprosta-5,13-dienoate.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane. May be  
 CC anchored to the membrane via a single transmembrane domain.  
 CC -1- SIMILARITY: Belongs to the cyclooxygenase P450 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC at the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: D30718; BA06383.1; -;  
 DR EMBL: L34208; AA53674.1; -;  
 DR EMBL: S67757; AB29680.1; -;  
 DR PIR: A53658; A53658.  
 DR InterPro: IPR001128; Cyclooxygenase\_P450.  
 DR InterPro: IPR002403; EP4501V.  
 DR Pfam: PF00067; P450; 2.  
 DR PRINTS: PR00465; EP4501V.  
 DR PRINTS: PR00385; P450.  
 DR PROSITE: PS00086; CYCLOOXYGENASE; Endoplasmic reticulum; Heme; Isomerase;  
 DR Direct protein sequencing; Endoplasmic reticulum; Heme; Isomerase;  
 KM Prostaglandin biosynthesis; Transmembrane.  
 FT TRANSMEM 1 20  
 FT METAL 441 441 Iron (heme axial ligand) (By similarity).  
 FT CONFLICT 192 192 S -> N (in Ref. 2).  
 FT CONFLICT 353 353 A -> P (in Ref. 2).  
 FT CONFLICT 407 407 N -> T (in Ref. 2).  
 FT SEQUENCE 500 AA; 56629 MW; 3738EEFEAE852403 CRC64;  
 SQ  
 Query Match 66.1%; Score 41; DB 1; Length 500;  
 Best Local Similarity 66.7%; Pred. No. 39;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GIEALPRTHSQ 12  
 DB 182 GVEALPHTQESQ 193  
 RESULT 12  
 Q87L51 PRELIMINARY; PRT; 802 AA.  
 AC Q87L51;  
 DT 01-JUN-2003 (TRENBLREL. 24, Created)  
 DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)  
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)  
 DE Aspartokinase II/homoserine dehydrogenase, methionine-sensitive.  
 GN OrderedLocusName=VP2764;

OS Vibrio parahaemolyticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=670;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RM221063 / Serotype O3:K6;  
 RX MEDLINE=22508454; PubMed=22620739; DOI=10.1016/S0140-6736(03)12659-1;  
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
 RA Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
 RA Yaenunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism  
 RT distinct from that of V. cholerae." J.  
 RL Lancet 361:743-749 (2003).  
 DR EMBL: AP005082; BAC61027.1; -;  
 DR HSPB; P31116; ISB.  
 DR GO: GO:0004072; F:aspartate kinase activity; IEA.  
 DR GO: GO:0004412; F:homoserine dehydrogenase activity; IEA.  
 DR GO: GO:0016301; F:kinase activity; IEA.  
 DR GO: GO:0016740; F:transferase activity; IEA.  
 DR GO: GO:0009067; P:aspartate family amino acid biosynthesis; IEA.  
 DR InterPro: IPR001048; As\_kinase.  
 DR InterPro: IPR001341; Aspartate\_kinase.  
 DR InterPro: IPR005106; Hmr\_dh\_NAD\_bind.  
 DR InterPro: IPR001342; Homoser\_dehydrog.  
 DR InterPro: IPR011147; Thra.  
 DR Pfam: PF00695; AA\_kinase; 1.  
 DR Pfam: PF00742; Homoserine\_dh; 1.  
 DR Pfam: PF03447; NAD\_binding\_3; 1.  
 DR PIRSF: PIRSF00727; Thra; 1.  
 DR TIGRFAMs: TIGR00657; asp\_kinases; 1.  
 DR PROSITE: PS00324; ASPARTOKINASE; UNKNOWN\_1.  
 DR PROSITE: PS01042; HOMOSER\_DHGENASE; 1.  
 KW Complete proteome; Kinase; Transferase.  
 SQ SEQUENCE 802 AA; 87817 MW; 255802A4F80F3D90 CRC64;  
 Query Match 66.1%; Score 41; DB 2; Length 802;  
 Best Local Similarity 77.8%; Pred. No. 65;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GIEALPRTH 9  
 DB 743 GVEALPREH 751  
 RESULT 13  
 Q92MI8 PRELIMINARY; PRT; 399 AA.  
 AC Q92MI8;  
 DT 01-DEC-2001 (TRENBLREL. 19, Created)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)  
 DE PUTATIVE TRANSPORT PROTEIN TRANSMEMBRANE.  
 GN ORFName=SMC00744;  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;  
 RA Capela D., Barloy-Hudler F., Gouzy T., Botne G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,  
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaune V., Maury D.,  
 RA Pohl T., Portetle D., Puehler A., Purnelle B., Rampeger U.,  
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021." J.  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).  
 DR EMBL: AL591791; CAC47207.1; -;  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0005215; F:transporter activity; IEA.

DR GO:0006810; P:transport; IEA.  
DR InterPro; IPR004812; EFLUX\_Bor\_CFLA.  
DR InterPro; IPR007114; MFS.  
DR Trifurcates; TIGR00710; efflux\_Bor\_CFLA; 1.  
DR PROSITE; PS50850; MFS; 1.  
KM Complete proteome; Transmembrane.  
SQ SEQUENCE 399 AA; 42519 MW; CD4E7453D34BDC89 CRC64;  
Query Match 64.5%; Score 40; DB 2; Length 399;  
Best Local Similarity 63.6%; Pred. No. 48;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 IEALPRTHEQ 12  
Db 184 LQALPRTHEQ 194  
RESULT 14  
Q9SVU3 PRELIMINARY; PRT; 880 AA.  
ID Q9SVU3  
AC Q9SVU3  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE Hypothetical protein F16A16.130 (Hypothetical protein AT4g28760).  
GN Name=F16A16.130; Synonyms=AT4g28760;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
OC NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Beyan M., Brandt P., Dose S., Jarke D., Scharfe M., Schon O.,  
RA Hoteisei J., Mewes H.W., Mayer K.F.X., Scheller C.,  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Brandt P., Dose S., Jarke D., Scharfe M., Schon O., Mewes H.W.,  
RA Lemcke K., Mayer K.F.X.,  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL035353; CAA22976.1; -  
DR EMBL; AL161573; CAB1464.1; -  
DR PIR; T04523; T04523.  
KM Hypothetical protein.  
SQ SEQUENCE 880 AA; 98423 MW; 5FD102587BCBFO CRC64;  
Query Match 64.5%; Score 40; DB 2; Length 880;  
Best Local Similarity 60.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GIEALPRTHE 10  
Db 44 GLETLPTQTHQ 53  
RESULT 15  
Q949M4 PRELIMINARY; PRT; 924 AA.  
ID Q949M4  
AC Q949M4  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE Hypothetical protein At4g28760.  
GN Name=At4g28760;

OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
OC NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,  
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Eckert J.R.,  
RA Theologis A.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,  
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,  
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,  
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Eckert J.R.,  
RA Theologis A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY051010; AAK93687.1; -  
DR EMBL; AY113649; AAM44897.1; -  
KM Hypothetical protein.  
SQ SEQUENCE 924 AA; 102903 MW; 10B55CC87876CA86 CRC64;  
Query Match 64.5%; Score 40; DB 2; Length 924;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GIEALPRTHE 10  
Db 118 GLETLPTQTHQ 127  
RESULT 16  
Q6RK33 PRELIMINARY; PRT; 2530 AA.  
ID Q6RK33  
AC Q6RK33  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Polyketide synthase.  
GN Name=PKS1;  
OS Mycosphaerella zeae-maydis.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;  
OC Dothideomycetes et Chaetochytriomycetes incertae sedis;  
OC Mycosphaerellaceae; Mycosphaerella.  
OC NCBI\_TaxID=259522;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14676319; DOI=10.1073/pnas.2532165100;  
RA Kroken S., Glass N.L., Taylor J.W., Yoder O.C., Turgeon B.G.;  
RT "Phylogenomic analysis of type I polyketide synthase genes in  
pathogenic and saprobic ascomycetes."  
RL Proc. Natl. Acad. Sci. U.S.A. 100:15670-15675(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Yun S.-Y., Turgeon B.G.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY95642; AAR8531.1; -  
DR GO:0004024; F:alcohol dehydrogenase activity; IEA.  
DR GO:0016740; F:transferase activity; IEA.  
DR GO:0008270; F:zinc ion binding; IEA.  
DR GO:0006633; P:fatty acid biosynthesis; IEA.  
DR GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR009081; ACP\_like.

DR InterPro; IPR001227; AC transferase.  
DR InterPro; IPR002085; Adh\_zn\_family.  
DR InterPro; IPR011032; GroES\_like.  
DR InterPro; IPR000794; Ketoacyl\_synth.  
DR InterPro; IPR006163; Phosphatase\_bind.  
DR InterPro; IPR006162; Ppantase\_S.  
DR Pfam; PF00698; Acyl\_transf\_1; 1.  
DR Pfam; PF00107; ADH\_zinc\_N; 1.  
DR Pfam; PF00109; ketoacyl-synt; 1.  
DR Pfam; PF02801; ketoacyl-synt\_C; 1.  
DR Pfam; PF00550; pp-binding; 1.  
DR PROSITE; PS00075; ACP DOMAIN; 1.  
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
DR Transferase.  
RW SEQUENCE 2530 AA; 274185 MW; 7EEC2008E6B8BF CRC64;  
SQ

Query Match 64.5%; Score 40; DB 2; Length 2530;  
Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EALPRTHSQ 12  
||| |||  
Db 1339 EALARTHEQ 1348

RESULT 17  
Q87XK6 PRELIMINARY; PRT; 248 AA.  
AC Q87XK6:  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Amino acid ABC transporter, permease protein.  
GN OrderedLocusNames=PSPT04172;  
OS Pseudomonas syringae (pv. tomato).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=323;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DCJ000.  
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;  
RA Buell C.R., Joarjar V., Lindeberg M., Selensut J., Paulsen I.T.,  
RA Gwin M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolony J.F.,  
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,  
RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,  
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,  
RA Ueberback T.R., Van Aken S.E., Feldblyum T.V., D'Accenzo M.,  
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,  
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,  
RA Bender C.L., White O., Fraser C.M., Collier A.,  
RT "The complete genome sequence of the Arabidopsis and tomato pathogen  
Pseudomonas syringae pv. tomato DCJ000".  
RT Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).  
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.  
CC Probably responsible for the translocation of the substrate across  
CC the membrane (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport  
CC system permease family.  
CC EMBL; AE016871; AA057628.1; -.  
DR TIGR; PSP04172; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR000515; BPD\_transp.  
DR InterPro; IPR010065; HEQRO\_ABC\_3TM.  
DR Pfam; PF00528; BPD\_transp\_1; 1.  
DR TIGRfams; TIGR01726; HEQRO\_perm\_3TM; 1.  
DR PROSITE; PS00928; ABC\_TM1; 1.  
RW Complete proteome; Transmembrane; Transport.  
KW Complete proteome; Transmembrane; Transport.  
SQ SEQUENCE 248 AA; 27601 MW; ADB9B7B38279BD CRC64;

Query Match 62.9%; Score 39; DB 2; Length 248;  
Best Local Similarity 72.7%; Pred. No. 44;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GIALPRTHS 11  
||| |||  
Db 133 GIALPQGES 143

RESULT 18  
Q9VAP7 PRELIMINARY; PRT; 271 AA.  
ID Q9VAP7:  
AC Q9VAP7:  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE CG17985-PA (LD36653p).  
DE CG17985-PA (LD36653p).  
GN ORFNames=CG17985;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.E., Vandeil M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazer V.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abtill J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,  
RA Butts K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Dou P.L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hooten D., Houston K.A., Howland T.J., Wei M.H., Ibegyan C.,  
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Palet J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheefel F., Shen H.,  
RA Shue B.C., Siden-Kimmo I., Simpson M., Skupski M.P., Smith T.,  
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskae R., Tector A.C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weinstein J.,  
RA Williams S.M., Woodgerl, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of Drosophila melanogaster".  
RT Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426055; PubMed=12537568;  
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champagne M., Dugan S.P., Fries E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacible J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskae R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Rubin G.M.,

RT "finishing a whole-genome shotgun: Release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence."  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomic perspective."  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Miura S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminler J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bertencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review."  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarini H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nunoo J., Paclib J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003840; AAF59218.1; -  
DR EMBL; AY051872; AAF32936.1; -  
DR InterPro: IPR002482; LysM.  
DR Pfam; PF01476; LysM; 1.  
DR SMART; SMO0257; LysM; 1.  
SQ SEQUENCE 271 AA; 30342 MW; 97EC5A4F937B2D60 CRC64;  
Query Match 62.9%; Score 39; DB 2; Length 271;  
Best Local Similarity 63.6%; Pred. No. 49;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GLEALPRTSES 11  
Db 114 GLEALPAVHRS 124  
RESULT 19  
0870G9 PRELIMINARY; PRT; 283 AA.  
AC 0870G9;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Putative lipase activator protein.  
OS OrderedLocustNames=VP1180;  
OS Vibrio parahaemolyticus;  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrrio.

OX NCBI\_TaxID=670;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RMWD 221063 / Serotype O3:K6;  
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;  
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
RA Iijima Y., Najiwa M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
RA Yaenaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism  
RT distinct from that of V. cholerae."  
RL Lancet 361:743-749(2003).  
DR EMBL; AP005077; BACS9443.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006457; F:protein folding; IEA.  
DR InterPro: IPR004961; Lipase\_chap.  
DR Pfam; PF02280; Lipase\_chap; 1.  
KW Complete proteome.  
SQ SEQUENCE 283 AA; 32685 MW; 512FDA348D6BCA1 CRC64;  
Query Match 62.9%; Score 39; DB 2; Length 283;  
Best Local Similarity 72.7%; Pred. No. 51;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 IEALPRTSESQ 12  
Db 272 IEALERIHDSQ 282  
RESULT 20  
06CKA0 PRELIMINARY; PRT; 294 AA.  
AC 06CKA0;  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE Similar to sp|P25605 Saccharomyces cerevisiae YCL009c IIIV  
DE acetoacetate synthase.  
GN ORFNames=KILAOF123649;  
OS Kluyveromyces fragilis NRRL Y-1140.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=2845590;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NRRL Y-1140;  
RG Genolevures;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
RA Boissrame A., Boyer J., Cartolico L., Confariolieri F., de Darvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropfi A.,  
RA Hantrege F., Hemequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicoud J.M., Nikoleki M., Oztas S., Ozler-Kalogropoulos O.,  
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Sureau A.,  
RA Swenne D., Tekala F., Mesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,  
RL "Genome evolution in yeasts."  
RT Nature 430:35-44(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NRRL Y-1140;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DE Summary;  
DR EMBL; CR382126; CAG98347.1; -  
DR GO; GO:0003984; F:acetoacetate synthase activity; IEA.  
DR GO; GO:0016587; F:amino acid binding; IEA.  
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR004789; Acolac\_synthsm.  
 DR InterPro; IPR002812; ACT.  
 DR InterPro; IPR010983; EF\_Hand\_like.  
 DR Pfam; PF01842; ACT; 1.  
 DR ProDom; PD002844; Acolac\_synthsm; 1.  
 DR TrEMBL; TR000119; acolac sm; 1.  
 SQ SEQUENCE 294 AA; 32714 MW; 0A8E456C6269ABD6 CRC64;

Query Match 62.9%; Score 39; DB 2; Length 294;  
 Best Local Similarity 72.7%; Pred. No. 53;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 G1EALPRTTHS 11  
 Db 261 GMMALPRTTHLS 271

## RESULT 21

ID Q73Y81 PRELIMINARY; PRT; 310 AA.  
 AC Q73Y81;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocNames=MAP2076c;  
 OS Mycobacterium paratuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 NCBI\_TaxId=1770;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=k10;  
 RC Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE017234; AAS04393.1;  
 DR InterPro; IPR003455; Omt\_N.  
 DR Pfam; PF02409; Omt\_N; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 310 AA; 33750 MW; D1BC2CF9C401F980 CRC64;

Query Match 62.9%; Score 39; DB 2; Length 310;  
 Best Local Similarity 54.5%; Pred. No. 57;  
 Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G1EALPRTTHS 11  
 Db 265 G1EALPRTTHS 295

## RESULT 22

ID Q6A8K2 PRELIMINARY; PRT; 364 AA.  
 AC Q6A8K2;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Ion channel membrane protein.  
 GN OrderedLocNames=PPA1165;  
 OS Propionibacterium acnes.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.  
 NCBI\_TaxId=1747;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=KPA171202 / DSM 16379;  
 RC PubMed=15286373; DOI=10.1126/science.1100330;  
 RA Bruggemann H., Henne A., Hostet F., Liesegang H., Wieser A.,  
 RA Strittmatter A., Hufner S., Hueter P., Gottschalk G.;  
 RT "The complete genome sequence of Propionibacterium acnes, a commensal  
 of human skin."  
 RL Science 305:671-673(2004).  
 DR EMBL; AE017283; AAT82914.1; -.

DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005267; F:potassium channel activity; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro; IPR001622; K-channel\_pore.  
 DR InterPro; IPR003148; TrKA\_N.  
 DR Pfam; PF02254; TrKA\_N; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 364 AA; 39918 MW; 52A0E90C7374596A CRC64;

Query Match 62.9%; Score 39; DB 2; Length 364;  
 Best Local Similarity 70.0%; Pred. No. 67;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EALPRTTHSQ 12  
 Db 348 KAVPRRHESQ 357

## RESULT 23

ID Q8XAU8 PRELIMINARY; PRT; 367 AA.  
 AC Q8XAU8; Q7AE18;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE 22221 protein (Oxygen sensing protein).  
 GN OrderedLocNames=Ecgs2093; 22221;  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 NCBI\_TaxId=83334;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=O157:H7 / EDJ933 / ATCC 700927 / EHEC;  
 RC MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."  
 RL Nature 409:529-533(2001).  
 RX [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=O157:H7 / RIMD 0509952 / EHEC;  
 RC MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 O157:H7 and genomic comparison with a laboratory strain K-12."  
 RL DNA Res. 8:11-22(2001).  
 DR EMBL; AE005356; AAG56280.1;  
 DR EMBL; AP002557; BAB35516.1;  
 DR PIR; D85727; D85727.  
 DR PIR; E90890; E90890.  
 DR InterPro; IPR001633; EAL.  
 DR InterPro; IPR000160; GGDEF.  
 DR Pfam; PF00563; EAL; 1.  
 DR Pfam; PF00990; GGDEF; 1.  
 DR SMART; SM00267; DUF1; 1.  
 DR SMART; SM00052; DUF2; 1.  
 DR PROSITE; PS50883; EAL; 1.  
 DR PROSITE; PS50887; GGDEF; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 367 AA; 41488 MW; 7C09FP9172711EB0 CRC64;

Query Match 62.9%; Score 39; DB 2; Length 367;  
 Best Local Similarity 66.7%; Pred. No. 68;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIEALPRTHESEQ 12  
 Db 142 GIEALPRTHESEQ 153

## RESULT 24

Q86L11 PRELIMINARY; PRT; 400 AA.  
 AC Q86L11;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.  
 NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX4;  
 RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;  
 RA Gloeckner G., Eichinger L., Szafranski K., Pachbat J., Dear P.,  
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,  
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,  
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";  
 RL Nature 418:79-85(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX4;  
 RA Baumgart C.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC117075; AAC050797.1; -  
 DR InterPro; IPR009457; DUF1084.  
 DR Pfam; PF06454; DUF1084; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 400 AA; 45637 MW; F973507E054D3014 CRC64;

Query Match 62.9%; Score 39; DB 2; Length 400;  
 Best Local Similarity 72.7%; Pred. No. 75;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 IEALPRTHESEQ 12  
 Db 209 IEALPRTHESEQ 219

## RESULT 25

Q9HC82 PRELIMINARY; PRT; 838 AA.  
 AC Q9HC82;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Rb-associated protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20403887; PubMed=10944455; DOI=10.1006/birc.2000.3242;  
 RA Wen H., Ao S.;  
 RT "REP95, a novel leucine zipper protein, binds to the retinoblastoma  
 RT protein.";  
 RL Biochem. Biophys. Res. Commun. 275:141-148(2000).  
 DR EMBL; AF122819; AAG13723.1; -  
 DR PIR; JC7363; JC7363.  
 SQ SEQUENCE 838 AA; 94780 MW; 1C8D20BAA1038348 CRC64;

Query Match 62.9%; Score 39; DB 2; Length 838;  
 Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 IEALPRTHESEQ 12

Db 105 VEALLRCHSEQ 115

## RESULT 26

Q6AHZ6 PRELIMINARY; PRT; 1001 AA.  
 AC Q6AHZ6;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Hypothetical protein DKFZp686K191.  
 GN Name=DKFZp686K191;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cervix;  
 RG The German CDNA Consortium;  
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
 RA Mees H.W., Weil B., Amd C., Oeinger A., Fob G., Han M., Wiemann S.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1-SIMILARITY: Contains 1 RING-type zinc finger.  
 DR EMBL; CR627431; CAH10518.1; -  
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0016567; F:protein ubiquitination; IEA.  
 DR InterPro; IPR01841; Znf\_fing.  
 DR Pfam; PF00097; ZF-C3HC4; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS00518; ZF\_RING\_1; 1.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 1001 AA; 113677 MW; DE71D881F328F83D CRC64;

Query Match 62.9%; Score 39; DB 2; Length 1001;  
 Best Local Similarity 72.7%; Pred. No. 2e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 IEALPRTHESEQ 12  
 Db 105 VEALLRCHSEQ 115

## RESULT 27

Q7L3T6 PRELIMINARY; PRT; 1001 AA.  
 AC Q7L3T6;  
 DT 05-JUN-2004 (TREMBlrel. 27, Created)  
 DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Ring finger protein 40, isoform 1.  
 GN Name=RNRF40;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, Skin, and Uterus;  
 RX MEDLINE=22386257; PubMed=12477937; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

```

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skelton U., Smalton D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maitra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strauberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; BC011769; AAH18647.1; -
DR EMBL; BC006133; AAH06133.1; -
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; ZF_C3HC4_1.
DR SMART; SM00184; RING_1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 1001 AA; 113677 MW; 408A6E5A9CC25E41 CRC64;

Query Match 62.9%; Score 39; DB 2; Length 1001;
Best Local Similarity 72.7%; Pred. No. 2e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 2 IEALPRTSESQ 12
DB 105 VEALLRCHESQ 115

RESULT 28
ID 075150 PRELIMINARY; PRT; 1030 AA.
AC 075150;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE KIAA0661 protein (Fragment).
GN Name=KIAA0661;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro."

```

```

RL DNA Res. 5:169-176(1998).
CC -1-SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AB014561; BAA31636.2; -
DR HSSP; P04268; IIC2.
DR Genew; HGNC:16867; RNF40.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; ZF_C3HC4_1.
DR SMART; SM00184; RING_1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
FT NON_TER 1
SQ SEQUENCE 1030 AA; 116351 MW; 8F0985AA9F500A96 CRC64;

Query Match 62.9%; Score 39; DB 2; Length 1030;
Best Local Similarity 72.7%; Pred. No. 2.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 2 IEALPRTSESQ 12
DB 134 VEALLRCHESQ 144

RESULT 29
ID 07YUM6 PRELIMINARY; PRT; 127 AA.
AC 07YUM6;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE ORFNames=TB927.2.5740;
GN Trypanosoma brucei.
OS Trypanosoma brucei.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22789168; PubMed=12907728; DOI=10.1093/nar/gkg673;
RA El-Sayed N.M.A., Ghedin E., Song J., MacLeod A., Brinkard F.,
RA Larkin C., Wanless D., Peterson J., Hou L., Taylor S., Tweedie A.,
RA Bileau N., Khalak H.G., Lin X., Mason T., Hamrick L., Catter E.,
RA Blandin G., Bartholomew D., Simpson A.J., Kaul S., Zhao H., Bai G.,
RA Van Aken S., Uterback T., Haas B., Koo H.L., Umayam L., Suh B.,
RA Gerrard C., Leech V., Qi R., Zhou S., Schwartz D., Feldblum T.,
RA Salzberg S., Tate A., Turner M.R., Vili E., White O., Melville S.,
RA Adams M.D., Fraser C.M., Donelson J.E.;
RT "The sequence and analysis of Trypanosoma brucei chromosome II."
RT Nucleic Acids Res. 31:4856-4863(2003).
DR EMBL; AE017170; AAQ16031.1; -
GN Hypothetical protein.
SQ SEQUENCE 127 AA; 14351 MW; A661A53F7948E7B CRC64;

Query Match 61.3%; Score 38; DB 2; Length 127;
Best Local Similarity 54.5%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 GIEALPRTSES 11
DB 24 GVSRLPRVHER 34

RESULT 30
ID 08CIT4 PRELIMINARY; PRT; 310 AA.
AC 08CIT4;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE BC023814 protein.

```

GN Name=BC023814;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stedman M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ugin T.B., Toshiyuki S., Carinci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smaltus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Straubeberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC023814; AAH23814.1; -.  
 DR MGI; MGI:2387197; BC023814.  
 SQ SEQUENCE 310 AA; 34271 MW; 121D28A1B471A032 CRC64;

Query March 61.3%; Score 38; DB 2; Length 310;  
 Best Local Similarity 50.0%; Pred. No. 88;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GIALPRTHE 10  
 | : : | | |  
 Db 296 GVGGIPRVTHE 305

Search completed: August 1, 2005, 08:48:19  
 Job time : 180 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 1, 2005, 08:39:44 ; Search time 42 Seconds  
(without alignments)  
21.328 Million cell updates/sec

Title: US-10-663-749-18  
Perfect score: 62  
Sequence: 1 GIEALPRTNHSQ 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

## Database : Issued Patents, AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCFUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	62	100.0	237 2 US-08-578-709-11	Sequence 11, Appl
2	62	100.0	500 2 US-08-578-709-15	Sequence 15, Appl
3	40	64.5	2584 3 US-08-936-135-4	Sequence 4, Appl
4	37	59.7	201 4 US-09-252-991A-19260	Sequence 19260, A
5	37	59.7	241 4 US-09-252-991A-20411	Sequence 20411, A
6	37	59.7	257 4 US-09-270-767-42280	Sequence 42280, A
7	37	59.7	392 4 US-09-902-540-13511	Sequence 13511, A
8	37	59.7	568 4 US-09-489-039A-10969	Sequence 10969, A
9	36	58.1	251 4 US-09-252-991A-21713	Sequence 21713, A
10	36	58.1	507 3 US-08-860-635A-19	Sequence 19, Appl
11	36	58.1	507 3 US-09-281-476-19	Sequence 19, Appl
12	36	58.1	509 3 US-09-910-087-19	Sequence 19, Appl
13	36	58.1	509 3 US-08-860-635A-21	Sequence 21, Appl
14	36	58.1	509 3 US-09-281-476-21	Sequence 21, Appl
15	36	58.1	509 3 US-09-910-087-21	Sequence 21, Appl
16	36	58.1	509 4 US-09-949-016-5930	Sequence 5930, Ap
17	36	58.1	531 4 US-09-252-991A-26690	Sequence 26690, A
18	36	58.1	556 4 US-09-949-016-9398	Sequence 9398, Ap
19	35	56.5	65 4 US-09-252-991A-11569	Sequence 11569, A
20	35	56.5	105 4 US-09-107-532A-6573	Sequence 6573, Ap
21	34	54.8	146 4 US-09-252-991A-11369	Sequence 11369, A
22	34	54.8	151 4 US-09-252-991A-22920	Sequence 22920, A
23	34	54.8	303 4 US-09-252-991A-22250	Sequence 22250, A
24	34	54.8	340 4 US-09-198-452A-362	Sequence 362, App
25	34	54.8	384 4 US-09-438-185A-347	Sequence 347, App
26	34	54.8	542 4 US-09-489-039A-9564	Sequence 9564, Ap
27	34	54.8	676 4 US-09-949-016-7426	Sequence 7426, Ap

28	34	54.8	700 4 US-09-252-991A-29072	Sequence 29072, A
29	34	54.8	1065 4 US-09-538-092-84	Sequence 84, Appl
30	34	54.8	1088 4 US-09-233-857-4	Sequence 4, Appl
31	34	54.8	2504 4 US-09-949-016-6454	Sequence 6454, Ap
32	33	53.2	123 4 US-09-270-767-61706	Sequence 61706, A
33	33	53.2	162 4 US-10-067-443-18	Sequence 18, Appl
34	33	53.2	203 4 US-09-248-796A-26241	Sequence 26241, A
35	33	53.2	241 4 US-09-270-767-59466	Sequence 59466, A
36	33	53.2	273 4 US-09-252-991A-20798	Sequence 20798, A
37	33	53.2	283 4 US-09-270-767-46148	Sequence 46148, A
38	33	53.2	295 4 US-09-252-991A-21169	Sequence 21169, A
39	33	53.2	313 4 US-09-902-540-14967	Sequence 14967, A
40	33	53.2	348 4 US-09-540-236-2479	Sequence 2479, Ap
41	33	53.2	360 4 US-09-252-991A-17645	Sequence 17645, A
42	33	53.2	360 4 US-09-270-767-44056	Sequence 44056, A
43	33	53.2	364 4 US-09-438-046-13	Sequence 13, Appl
44	33	53.2	386 4 US-09-538-092-1360	Sequence 1360, Ap
45	33	53.2	387 1 US-08-713-828-3	Sequence 3, Appl
46	33	53.2	387 2 US-08-919-627-3	Sequence 3, Appl
47	33	53.2	387 2 US-09-096-245-3	Sequence 30, Appl
48	33	53.2	387 3 US-09-457-0408-30	Sequence 5, Appl
49	33	53.2	388 1 US-08-713-828-5	Sequence 5, Appl
50	33	53.2	388 2 US-08-919-627-5	Sequence 5, Appl
51	33	53.2	388 2 US-09-096-245-5	Sequence 552, App
52	33	53.2	394 4 US-09-710-279-552	Sequence 31550, A
53	33	53.2	409 4 US-09-252-991A-31550	Sequence 7693, Ap
54	33	53.2	428 4 US-09-543-681A-7693	Sequence 3148, Ap
55	33	53.2	443 3 US-09-134-010C-3148	Sequence 3148, Ap
56	33	53.2	473 4 US-09-270-767-37633	Sequence 37633, A
57	33	53.2	473 4 US-09-270-767-52850	Sequence 52850, A
58	33	53.2	519 4 US-08-956-171E-5230	Sequence 5230, Ap
59	33	53.2	519 4 US-08-781-986A-5230	Sequence 5230, Ap
60	33	53.2	536 4 US-09-902-540-13091	Sequence 13091, A
61	33	53.2	570 4 US-09-248-766A-19123	Sequence 19123, A
62	33	53.2	577 4 US-09-107-532A-5217	Sequence 5217, Ap
63	33	53.2	595 3 US-08-842-079-6	Sequence 6, Appl
64	33	53.2	595 3 US-08-842-079-17	Sequence 17, Appl
65	33	53.2	595 4 US-09-638-857-6	Sequence 6, Appl
66	33	53.2	595 4 US-09-638-857-17	Sequence 17, Appl
67	33	53.2	645 4 US-09-315-127-8	Sequence 9, Appl
68	33	53.2	645 4 US-09-315-127-9	Sequence 9, Appl
69	33	53.2	671 4 US-09-252-991A-23611	Sequence 23611, A
70	33	53.2	774 4 US-09-252-991A-16789	Sequence 16789, A
71	33	53.2	854 4 US-09-252-991A-18848	Sequence 18848, A
72	33	53.2	1039 4 US-09-252-991A-28966	Sequence 28966, A
73	32	51.6	141 4 US-09-270-767-36726	Sequence 36726, A
74	32	51.6	141 4 US-09-270-767-51943	Sequence 51943, A
75	32	51.6	151 4 US-09-543-681A-6296	Sequence 6296, Ap
76	32	51.6	151 4 US-09-543-681A-7365	Sequence 7365, Ap
77	32	51.6	156 4 US-09-543-681A-5578	Sequence 5578, Ap
78	32	51.6	156 4 US-09-543-681A-6342	Sequence 6342, Ap
79	32	51.6	156 4 US-09-543-681A-7162	Sequence 7162, Ap
80	32	51.6	156 4 US-09-543-681A-7328	Sequence 7328, Ap
81	32	51.6	156 4 US-09-489-039A-8616	Sequence 8616, Ap
82	32	51.6	156 4 US-09-489-039A-9028	Sequence 9028, Ap
83	32	51.6	156 4 US-09-489-039A-11772	Sequence 11772, A
84	32	51.6	156 4 US-09-489-039A-11803	Sequence 11803, A
85	32	51.6	156 4 US-09-489-039A-12651	Sequence 12651, A
86	32	51.6	156 4 US-09-489-039A-13713	Sequence 13713, A
87	32	51.6	164 4 US-09-711-164-4-73	Sequence 373, App
88	32	51.6	192 4 US-09-485-632B-2	Sequence 2, Appl
89	32	51.6	219 4 US-09-270-767-57118	Sequence 57118, A
90	32	51.6	247 4 US-09-248-766A-14828	Sequence 14828, A
91	32	51.6	307 4 US-09-902-540-10505	Sequence 10505, A
92	32	51.6	320 4 US-09-252-991A-23942	Sequence 23942, A
93	32	51.6	323 4 US-09-270-767-18794	Sequence 18794, A
94	32	51.6	351 4 US-09-857-447-1	Sequence 1, Appl
95	32	51.6	361 4 US-09-270-767-42397	Sequence 42397, A
96	32	51.6	362 4 US-09-252-991A-17884	Sequence 17884, A
97	32	51.6	372 4 US-09-252-991A-28851	Sequence 28851, A
98	32	51.6	386 4 US-09-270-767-41615	Sequence 41615, A
99	32	51.6	402 4 US-09-538-092-349	Sequence 349, App
100	32	51.6	424 4 US-09-252-991A-18784	Sequence 18784, A



```

; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-578-709-15

Query Match          100.0%; Score 62; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GIEALPRTHSQ 12
        |||||
Db       182 GIEALPRTHSQ 193

RESULT 3
US-08-936-135-4
; Sequence 4, Application US/08936135
; Patent No. 6054293
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: He, Zhigang
; APPLICANT: Chen, Hang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2584 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-936-135-4

Query Match          64.5%; Score 40; DB 3; Length 2584;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 GIEALPRTHS 11
        |||||
Db       1636 GVALPRTHRA 1646

RESULT 4
US-09-252-991A-19260
; Sequence 19260, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19260
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19260

Query Match          59.7%; Score 37; DB 4; Length 201;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GIEALPRTH 9
        |||||
Db       172 GLRTLPRTH 180

RESULT 5
US-09-252-991A-20411
; Sequence 20411, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20411
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20411

Query Match          59.7%; Score 37; DB 4; Length 241;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GIEALPRTH 10
        |||||
Db       141 GQAARPTH 150

RESULT 6
US-09-270-767-42280
; Sequence 42280, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 42280
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
```

US-09-270-767-42280

Query Match 59.7%; Score 37; DB 4; Length 257;

Best Local Similarity 66.7%; Pred. No. 48; Indels 1; Gaps 0;

Matches 6; Conservative 2; Mismatches 1;

Qy 2 IEALPRTHE 10

Db 83 LEALPRLHE 91

RESULT 7

US-09-902-540-13511

Sequence 13511, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 13511

LENGTH: 392

TYPE: PRT

ORGANISM: Myxococcus xanthus

US-09-902-540-13511

Query Match 59.7%; Score 37; DB 4; Length 392;

Best Local Similarity 54.5%; Pred. No. 76; Indels 1; Gaps 0;

Matches 6; Conservative 4; Mismatches 1;

Qy 2 IEALPRTHESQ 12

Db 166 LQALPRMHETR 176

RESULT 8

US-09-489-039A-10969

Sequence 10969, Application US/09489039A

Patent No. 6610835

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

FILE REFERENCE: 2709.2004001

CURRENT FILING DATE: 2000-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 10969

LENGTH: 568

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-10969

Query Match 59.7%; Score 37; DB 4; Length 568;

Best Local Similarity 58.3%; Pred. No. 1.1e+02; Indels 0; Gaps 0;

Matches 7; Conservative 2; Mismatches 3;

Qy 1 GIEALPRTHESQ 12

Db 422 GIEVVRRLHQSO 433

RESULT 9

US-09-252-991A-21713

Sequence 21713, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21713

LENGTH: 251

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21713

Query Match 58.1%; Score 36; DB 4; Length 251;

Best Local Similarity 66.7%; Pred. No. 71; Indels 2; Gaps 0;

Matches 6; Conservative 1; Mismatches 2;

Qy 2 IEALPRTHE 10

Db 20 VEQAPRTHE 28

RESULT 10

US-08-860-635A-19

Sequence 19, Application US/08860635A

Patent No. 6143878

GENERAL INFORMATION:

APPLICANT: Koopman, Peter

APPLICANT: Goodfellow, Peter

TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSER: Scully, Scott, Murphy &amp; Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: NY

COUNTRY: U.S.A.

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/860.635A

FILING DATE: 29-MAY-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PM9714

FILING DATE: 29-NOV-1994

APPLICATION NUMBER: AU PM9835

FILING DATE: 05-DEC-1994

APPLICATION NUMBER: PCT/AU95/00799

FILING DATE: 29-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: DiGiiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 10981

TELECOMMUNICATION INFORMATION:

TELEPHONE: 516-742-4343

TELEFAX: 516-742-4366

TELEX:

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-860-635A-19

Query Match 58.1%; Score 36; DB 3; Length 507;  
Best Local Similarity 41.7%; Pred. No. 1.5e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GREALPRTHEQ 12  
|:|:|:|:|:|  
Db 483 GVPSIPQTHSPQ 494

RESULT 11  
; Sequence 19, Application US/09281476  
; Patent No. 6316597  
; GENERAL INFORMATION:  
; APPLICANT: Koopman, Peter  
; APPLICANT: Goodfellow, Peter  
; TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND  
; TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/281,476  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/860,635  
; FILING DATE:  
; APPLICATION NUMBER: AU PM9835  
; FILING DATE: 05-DEC-1994  
; APPLICATION NUMBER: PCT/AU95/00799  
; FILING DATE: 29-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DIGI9110, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 10981  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 507 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; US-09-281-476-19

Query Match 58.1%; Score 36; DB 3; Length 507;  
Best Local Similarity 41.7%; Pred. No. 1.5e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GREALPRTHEQ 12  
|:|:|:|:|:|  
Db 483 GVPSIPQTHSPQ 494

RESULT 12  
; US-09-910-087-19  
; Sequence 19, Application US/09910087  
; Patent No. 6737413  
; GENERAL INFORMATION:  
; APPLICANT: Koopman, Peter  
; APPLICANT: Goodfellow, Peter  
; TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND  
; TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/910,087  
; FILING DATE: 20-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PM9714  
; FILING DATE: 29-NOV-1994  
; APPLICATION NUMBER: AU PM9835  
; FILING DATE: 05-DEC-1994  
; APPLICATION NUMBER: PCT/AU95/00799  
; FILING DATE: 29-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DIGI9110, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 10981  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 507 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: <Unknown>  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
; US-09-910-087-19

Query Match 58.1%; Score 36; DB 4; Length 507;  
Best Local Similarity 41.7%; Pred. No. 1.5e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GREALPRTHEQ 12  
|:|:|:|:|:|  
Db 483 GVPSIPQTHSPQ 494

RESULT 13  
; US-08-860-635A-21  
; Sequence 21, Application US/08860635A  
; Patent No. 6143878  
; GENERAL INFORMATION:  
; APPLICANT: Koopman, Peter  
; APPLICANT: Goodfellow, Peter  
; TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND  
; TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser

Query Match 58.1%; Score 36; DB 3; Length 507;  
Best Local Similarity 41.7%; Pred. No. 1.5e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,635A  
FILING DATE: 29-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PM9714  
FILING DATE: 29-NOV-1994  
APPLICATION NUMBER: AU PM9835  
FILING DATE: 05-DEC-1994  
APPLICATION NUMBER: PCT/AU95/00799  
FILING DATE: 29-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10981  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
TELEX:  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 509 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-860-635A-21

Query Match 58.1%; Score 36; DB 3; Length 509;  
Best Local Similarity 41.7%; Pred. No. 1.5e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTHESEQ 12  
|:|:|:|:|  
Db 485 GVPSIPQTHSPQ 496

RESULT 14  
US-09-281-476-21  
Sequence 21, Application US/09281476  
Patent No. 6316597  
GENERAL INFORMATION:  
APPLICANT: Koopman, Peter  
APPLICANT: Goodfellow, Peter  
TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND  
TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/281,476  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/860,635  
FILING DATE:  
APPLICATION NUMBER: AU PM9835  
FILING DATE: 05-DEC-1994  
APPLICATION NUMBER: PCT/AU95/00799  
FILING DATE: 29-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10981  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
TELEX:  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 509 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-281-476-21

Query Match 58.1%; Score 36; DB 3; Length 509;  
Best Local Similarity 41.7%; Pred. No. 1.5e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTHESEQ 12  
|:|:|:|:|  
Db 485 GVPSIPQTHSPQ 496

RESULT 15  
US-09-910-087-21  
Sequence 21, Application US/09910087  
Patent No. 6737413  
GENERAL INFORMATION:  
APPLICANT: Koopman, Peter  
APPLICANT: Goodfellow, Peter  
TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND  
TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/910,087  
FILING DATE: 20-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PM9714  
FILING DATE: 29-NOV-1994  
APPLICATION NUMBER: AU PM9835  
FILING DATE: 05-DEC-1994  
APPLICATION NUMBER: PCT/AU95/00799  
FILING DATE: 29-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10981  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366

TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 509 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-910-087-21

Query Match 58.1%; Score 36; DB 4; Length 509;  
Best Local Similarity 41.7%; Pred. No. 1.5e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 G1EALPRTHEQ 12  
Db 485 GVPSP1QTHSPQ 496

RESULT 16  
US-09-949-016-5930  
; Sequence 5930, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5930  
; LENGTH: 509  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-5930

Query Match 58.1%; Score 36; DB 4; Length 509;  
Best Local Similarity 41.7%; Pred. No. 1.5e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 G1EALPRTHEQ 12  
Db 485 GVPSP1QTHSPQ 496

RESULT 17  
US-09-252-991A-26690  
; Sequence 26690, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26690  
; LENGTH: 531  
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26690

Query Match 58.1%; Score 36; DB 4; Length 531;  
Best Local Similarity 47.5%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1EALPRT 8  
Db 471 G1EALPRT 478

RESULT 18  
US-09-949-016-9398  
; Sequence 9398, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9398  
; LENGTH: 536  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9398

Query Match 58.1%; Score 36; DB 4; Length 536;  
Best Local Similarity 41.7%; Pred. No. 1.7e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 G1EALPRTHEQ 12  
Db 532 GVPSP1QTHSPQ 543

RESULT 19  
US-09-252-991A-31569  
; Sequence 31569, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 31569  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31569

Query Match 56.5%; Score 35; DB 4; Length 65;  
Best Local Similarity 63.6%; Pred. No. 25;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 G1EALPRTHEQ 11

Db 11 GABAPRTHRS 21

RESULT 20  
US-09-107-532A-6573  
Sequence 6573, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Atinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 6573:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...105  
SEQUENCE DESCRIPTION: SEQ ID NO: 6573:  
US-09-107-532A-6573

Query Match 54.8%; Score 34; DB 4; Length 105;  
Best Local Similarity 58.3%; Pred. No. 65;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIEALPRTHEQ 12  
|||:|:|:  
Db 52 GIPFLPRHPER 63

RESULT 21  
US-09-252-991A-31369  
Sequence 31369, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 31142  
;; SEQ ID NO 31369  
;; LENGTH: 146  
;; TYPE: PRT  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31369

Query Match 54.8%; Score 34; DB 4; Length 146;  
Best Local Similarity 50.0%; Pred. No. 92;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTHEQ 12  
|||:|:|:  
Db 38 GAEAVPQTEKR 49

RESULT 22  
US-09-252-991A-22920  
Sequence 22920, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 31142  
SEQ ID NO 22920  
LENGTH: 151  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22920

Query Match 54.8%; Score 34; DB 4; Length 151;  
Best Local Similarity 50.0%; Pred. No. 96;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIEALPRTHEQ 12  
|||:|:|:  
Db 129 GILQLPRHQOQ 140

RESULT 23  
US-09-252-991A-22250  
Sequence 22250, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 31142  
SEQ ID NO 22250  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22250

Query Match  
Best Local Similarity 54.8%; Score 34; DB 4; Length 303;  
Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IEALPRTH 9  
DB 138 VEALPRGH 145

RESULT 24

US-09-198-452A-362  
; Sequence 362, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffeid, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; FILE REFERENCE: 9710-003-999  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 362  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-362

Query Match  
Best Local Similarity 54.8%; Score 34; DB 4; Length 340;  
Pred. No. 2.3e+02;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTHS 11  
DB 61 GIEALPALES 71

RESULT 25

US-09-438-185A-347  
; Sequence 347, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; TITLE OF INVENTION: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 347  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: CPN0345  
US-09-438-185A-347

Query Match  
Best Local Similarity 54.8%; Score 34; DB 4; Length 384;  
Pred. No. 2.6e+02;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTHS 11  
DB 11111111 11

DB 105 GIEALPALES 115

RESULT 26  
US-09-489-039A-9564  
; Sequence 9564, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gaty Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 9564  
; LENGTH: 542  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-9564

Query Match  
Best Local Similarity 54.8%; Score 34; DB 4; Length 542;  
Pred. No. 3.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 ALPRTHSEQ 12  
DB 511 ALPRTHNGK 519

RESULT 27

US-09-949-016-7426  
; Sequence 7426, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7426  
; LENGTH: 676  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7426

Query Match  
Best Local Similarity 54.8%; Score 34; DB 4; Length 676;  
Pred. No. 4.8e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPRTHSEQ 12  
DB 424 LPRPHEAQ 431

RESULT 28

US-09-252-991A-29072  
; Sequence 29072, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

```
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23072
; LENGTH: 700
; TYPE: PRN
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29072
```

```
Query Match          54.8%; Score 34; DB 4; Length 700;
Best Local Similarity 60.0%; Pred. No. 5e+02;      2; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IEALPRTES 11
        :||:|||||
Db      213 LEAVPDHES 222
```

```
RESULT 29
US-09-538-092-84
; Sequence 84, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glaxo, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 84
; LENGTH: 1065
; TYPE: PRN
; ORGANISM: Saccharomyces cerevisiae
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number YCR067C
US-09-538-092-84
```

```
Query Match          54.8%; Score 34; DB 4; Length 1065;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;      3; Indels 0; Gaps 0;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IEALPRTES 11
        :||:|||||
Db      296 VQVPRVHES 305
```

```
RESULT 30
US-09-233-857-4
; Sequence 4, Application US/09233857
; Patent No. 6495353
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Flanagan, Peter
; TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
; FILE REFERENCE: 239/251
; CURRENT APPLICATION NUMBER: US/09/233,857
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: USSN 60/072,023
; EARLIER FILING DATE: 1998-01-21
```

```
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1088
; TYPE: PRN
; ORGANISM: HUMAN
US-09-233-857-4
```

```
Query Match          54.8%; Score 34; DB 4; Length 1088;
Best Local Similarity 66.7%; Pred. No. 8e+02;      1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 GIEALPRT 9
        :||:|||||
Db      385 GIEAPPPRAH 393
```

```
Search completed: August 1, 2005, 08:49:47
Job time : 44 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 1, 2005, 08:25:53 ; Search time 164 Seconds  
(without alignments)  
28.300 Million cell updates/sec

Title: US-10-663-749-18  
Perfect score: 62  
Sequence: 1 GIEALPRTMSQ 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database: A\_Geneseq\_16Dec04:\*

1: geneseqp19808:\*\n2: geneseqp19908:\*\n3: geneseqp20008:\*\n4: geneseqp20018:\*\n5: geneseqp20028:\*\n6: geneseqp20038:\*\n7: geneseqp20048:\*\n8: geneseqp20058:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	237	2	AAR84562 Human pro
2	62	100.0	500	2	AAR84561 Human pro
3	62	100.0	500	7	ADB70342 Proctacyc
4	62	100.0	500	8	ADJ37121 Human mal
5	40	64.5	739	8	ADP64397 Trichoder
6	39	62.9	147	4	AAU50660 Propionib
7	39	62.9	147	6	ABM47179 Propionib
8	39	62.9	147	4	ABM65595 Drosophil
9	39	62.9	420	4	AAU63605 Propionib
10	39	62.9	420	6	ABM60124 Propionib
11	39	62.9	948	8	ADJ37227 Human nuc
12	38	61.3	509	8	ABD11798 Human CGI
13	38	61.3	765	8	ADP64400 Trichoder
14	37	59.7	201	7	ABO70514 Pseudomon
15	37	59.7	241	7	ABO71665 Pseudomon
16	37	59.7	307	4	ABBS8234 Drosophil
17	37	59.7	410	6	ABO00565 Novel hum
18	37	59.7	568	7	ABO64452 Klebsiell
19	36	58.1	126	5	ABP41544 Human ova
20	36	58.1	152	6	ABM69852 Photorhab
21	36	58.1	152	6	ABM69781 Photorhab
22	36	58.1	179	8	ADK16367 Nanoarcha
23	36	58.1	198	4	AAW40723 Pseudomon
24	36	58.1	251	7	ABO72967 Pseudomon
25	36	58.1	336	6	ABU21788 Protein e

26	36	58.1	365	4	AAB65995 Human sec
27	36	58.1	366	4	AAB65996 Human sec
28	36	58.1	403	8	ADG22625 Bacterial
29	36	58.1	403	8	ADG25515 Bacterial
30	36	58.1	403	8	ADG26083 Bacterial
31	36	58.1	509	2	AAR97646 Human SOX
32	36	58.1	509	2	AAR97645 Mouse Sox
33	36	58.1	509	8	ADQ19665 Human sof
34	36	58.1	531	7	ABO77944 Pseudomon
35	36	58.1	546	5	ABP28539 Streptoco
36	36	58.1	546	5	ABP28539 Streptoco
37	36	58.1	571	6	ABR01339 Human gen
38	36	58.1	571	6	ABR01339 Human gen
39	36	58.1	572	4	AAAB65936 Human sec
40	36	58.1	592	4	ABBS58841 Drosophil
41	36	58.1	756	6	ABR01092 Human gen
42	36	58.1	756	7	ADG20413 Human sec
43	36	58.1	1076	6	ABU11363 Protein e
44	36	58.1	1076	6	ABU11363 Protein e
45	36	58.1	1770	4	AAAB39102 Human pol
46	36	58.1	1805	4	ABG04010 Novel hum
47	36	58.1	1848	4	AAW40888 Human pol
48	35	56.5	227	2	AAV35592 Fragment
49	35	56.5	227	6	ADAL1762 Human nov
50	35	56.5	65	7	ABO82823 Pseudomon
51	35	56.5	118	4	AAU48071 Propionib
52	35	56.5	149	6	ABM44590 Propionib
53	35	56.5	149	6	ABU21933 Protein e
54	35	56.5	244	8	ADG23974 Bacterial
55	35	56.5	317	4	AAAB7538 Burkholde
56	35	56.5	347	8	ADQ67678 Novel hum
57	35	56.5	439	6	ADAL1755 Human nov
58	35	56.5	470	8	ADG27952 Bacterial
59	35	56.5	555	7	ADB64376 Human pro
60	35	56.5	598	8	ADN21438 Bacterial
61	35	56.5	703	6	ABU24041 Protein e
62	35	56.5	1274	4	AAAB7329 FcTR6. 8/
63	35	56.5	1498	5	ABBA48222 Listeria
64	34	54.8	64	6	ABP34128 Human ORF
65	34	54.8	64	6	ABP80296 N. gonorr
66	34	54.8	67	5	ABG46802 Human pep
67	34	54.8	69	4	AAAB7340 Human imm
68	34	54.8	86	4	AAU59052 Propionib
69	34	54.8	86	6	ABM55571 Propionib
70	34	54.8	91	5	ABP32541 Human ORF
71	34	54.8	100	5	ADP32644 Human tra
72	34	54.8	105	7	ADG96946 E. faeciu
73	34	54.8	106	4	ABB68525 Drosophil
74	34	54.8	113	6	ABR41351 Human DIT
75	34	54.8	146	7	ABO82623 Pseudomon
76	34	54.8	147	4	AAAB83078 Human imm
77	34	54.8	150	4	AAU58191 Propionib
78	34	54.8	150	6	ABM54710 Propionib
79	34	54.8	151	7	ABO74174 Pseudomon
80	34	54.8	157	8	ADQ79657 Aspergill
81	34	54.8	171	2	AAW60240 Human pro
82	34	54.8	171	2	AAW60242 Human pro
83	34	54.8	171	2	AAW60241 Human pro
84	34	54.8	171	7	ADG56795 Human pro
85	34	54.8	171	7	ADG56799 Human pro
86	34	54.8	171	7	ADG56803 Human pro
87	34	54.8	180	8	ADP90893 Human pha
88	34	54.8	180	8	ADP90893 Human pha
89	34	54.8	195	8	ADP68380 Border di
90	34	54.8	206	8	ADP85041 Human ato
91	34	54.8	206	8	ADP85041 Human ato
92	34	54.8	239	4	AAU30328 Novel hum
93	34	54.8	263	6	ABU25370 Aspergill
94	34	54.8	303	6	ABU43795 Protein e
95	34	54.8	303	6	ABU43795 Protein e
96	34	54.8	313	7	ABU25370 Aspergill
97	34	54.8	315	6	ADG10775 Human the
98	34	54.8	327	8	ABM83540 Human dia

PT	Peptide	1..237	
FT		/note="prostagacyclin-synthase (AA 1-237) "	
XX			
FN	W09530013-A1.		
PD	09-NOV-1995.		
XX			
PF	27-APR-1995;	95MO-JP000838.	
XX			
PR	28-APR-1994;	94JP-00114316.	
XX			
PA	(TANA/) TANABE T.		
XX			
FI	Tanabe T;		
XX			
DR	WPI; 1995-393084/50.		
DR	N-PSDB; AAT05324.		
XX			
PT	Human prostacyclin synthase and DNA encoding it - useful in the		
PT	investigation and treatment of diseases characterised by reduced		
PT	prostaglandin I2 production.		
XX			
PS	Disclosure; Page 36-38; 71pp; Japanese.		
XX			
CC	Prostacyclin-synthase may be produced by recombinant DNA methods and		
CC	administered to patients to increase prostaglandin I2 (PGI2) production		
CC	to treat diseases characterized by reduced PGI2 levels or by an imbalance		
CC	between PGI2 and thromboxane A2 levels, such as circulatory diseases		
CC	(thrombosis, angina pectoris, arteriosclerosis, myocardial infarction).		
CC	The DNA and protein are also useful in disease diagnosis		
XX			
SQ	Sequence 237 AA;		
	Query Match	100.0%;	Score 62; DB 2; Length 237;
	Best Local Similarity	100.0%;	Pred. No. 0.0032;
	Matches 12; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 GIEALPRTHEsq 12		
	182 GIEALPRTHEsq 193		
DB			
RESULT 2			
AA84561			
ID	AA84561 standard; protein; 500 AA.		
XX			
AC	AA84561;		
XX			
DT	13-APR-1996 (first entry)		
XX			
DE	Human prostacyclin-synthase.		
XX			

	Key	Location/Qualifiers
FH	Peptide	1..237
FT		/note="clone pHPGIS36 (see AAR84562)"
FT	Peptide	225..285
FT		/note="clone phage lambda hPGIS141 (see AAR84564)"
FT	Peptide	226..500
FT		/note="clone pHPGIS135 (see AAR84563)"
XX		
XX		
PN	W09530013-A1.	
XX		
PD	09-NOV-1995.	
XX		
XX		
PF	27-APR-1995;	95WO-JP000838.
XX		
XX		
PR	28-APR-1994;	94JP-00114316.
XX		



CC squamous carcinoma, medulloblastoma, prostate cancer, breast cancer,  
CC diffuse large B-cell lymphoma, follicular lymphoma and ovarian cancer.  
CC The method is useful for diagnosing MPW in a subject suspected of having  
CC MPW which involves obtaining a tissue sample suspected of being cancerous  
CC from a subject and determining the expression of nucleic acid markers or  
CC its expression products in the tissue sample. This sequence represents a  
CC human MPW protein of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification but was obtained in  
CC electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX

SQ Sequence 500 AA;

Query Match 100.0%; Score 62; DB 8; Length 500;  
Best Local Similarity 100.0%; Pred. No. 0.007;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 1 G1EALPRTHEQ 12  
|||  
Db 182 G1EALPRTHEQ 193

RESULT 5  
ADP64397  
ID ADP64397 standard; protein; 739 AA.

XX ADP64397;

DT 12-AUG-2004 (first entry)

XX Trichoderma reesei beta-glucosidase BGL7 mature protein.

KW Beta-glucosidase; BGL7; yeast dough; baked food; detergent; aroma; wine;  
KW cellulase; biomass; bio-ethanol; enzyme; EC 3.2.1.21.

XX Hypocrea jecorina.

XX Key Location/Qualifiers

FT Misc-difference 7 /note= "Encoded by ATA codon of the sequences {seqid:1}  
FT and {seqid:4}"

FT Misc-difference 27 /note= "Encoded by GGC codon of the sequence {seqid:1}"

FT Misc-difference 61 /note= "Encoded by CT codon of the sequence {seqid:1}"

FT Misc-difference 66 /note= "Encoded by GGC codon of the sequence {seqid:1}"

FT Misc-difference 152 /note= "Encoded by MC codon of the sequence {seqid:1} and  
FT AAG codon of the sequence {seqid:4}"

FT Misc-difference 182 /note= "Encoded by GGC codon of the sequence {seqid:1}"

FT Misc-difference 193 /note= "Encoded by ATG codon of the sequence {seqid:4}"

FT Misc-difference 240 /note= "Encoded by TC codon of the sequence {seqid:1}"

FT Misc-difference 249 /note= "Encoded by TC codon of the sequence {seqid:1}"

FT Misc-difference 265 /note= "Encoded by GGC codon of the sequence {seqid:4}"

FT Misc-difference 376 /note= "Encoded by GGC codon of the sequence {seqid:4}"

FT Misc-difference 382 /note= "Encoded by TAG codon of the sequence {seqid:1}"

FT Misc-difference 401 /note= "Encoded by GGC codon of the sequence {seqid:1}"

FT Misc-difference 437 /note= "Encoded by GGT codon of the sequence {seqid:1}"

FT Misc-difference 473 /note= "Encoded by CGG codon of the sequence {seqid:1}"

FT Misc-difference 490 /note= "Encoded by TTCATCAAT codons of the sequences  
FT {seqid:1} and {seqid:4}"

FT Misc-difference 556 /note= "Encoded by TT codon of the sequence {seqid:4}"

FT /note= "Encoded by AA codon of the sequence {seqid:1}"  
FT Misc-difference 594 /note= "Encoded by GTC codon of the sequence {seqid:4}"  
FT Misc-difference 679 /note= "Encoded by GGC codon of the sequence {seqid:4}"  
FT Misc-difference 682 /note= "Encoded by AAG codon of the sequence {seqid:1}"  
FT Misc-difference 715 /note= "Encoded by TT codon of the sequence {seqid:1}"  
FT Misc-difference 729 /note= "Encoded by GGC codon of the sequence {seqid:4}"

XX US2004102619-A1.

XX 27-MAY-2004.

XX 21-NOV-2002; 2002US-00301015.

XX 21-NOV-2002; 2002US-00301015.

XX (DUNN/) DUNN-COLEMAN N.

XX (WARD/) WARD M.

XX Dunn-Coleman N, Ward M;

XX WPI; 2004-399738/37.

XX N-PSDB; ADP64396, ADP64399.

XX Novel BGL7 polypeptide having beta glucosidase activity useful for  
XX improving yeast dough or baked good made from such dough, for preparing  
XX detergent compositions or for enhancing potential aroma finished wine  
XX product.

XX Claim 18; SEQ ID NO 2; 25pp; English.

XX The invention relates to beta-glucosidase BGL7 (EC 3.2.1.21) polypeptide  
XX and polynucleotide from trichoderma. The enzyme is useful for improving  
XX the characteristics of a yeast dough or baked good made from such dough,  
XX for preparing detergent composition, for enhancing the potential aroma of  
XX finished wine product, for hydrolysis of cellulose to its sugar  
XX components, for preparing cellulase composition for use in detergents or  
XX for degradation of biomass into sugar for bio-ethanol production. The  
XX present sequence is trichoderma reesei beta-glucosidase BGL7 mature  
XX protein.

SQ Sequence 739 AA;

Query Match 64.5%; Score 40; DB 8; Length 739;  
Best Local Similarity 58.3%; Pred. No. 1.4e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Gy 1 G1EALPRTHEQ 12  
|||  
Db 3 GVSQLPSTHSSQ 14

RESULT 6  
AAU50660  
ID AAU50660 standard; protein; 147 AA.

XX AAU50660;

DT 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #11556.

XX SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;  
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
XX dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX

[illegible]

OS Drosophila melanogaster.  
XX  
XX WO200171042-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US009231.  
XX  
XX 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
PI  
XX WPI: 2001-6556860/75.  
DR N-PSDB; ABL10698.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
XX interactions.  
XX  
XX Disclosure; SEQ ID NO 26577; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signaling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-  
CC ABBS2072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 271 AA;  
SQ  
Query Match 62.9%; Score 39; DB 4; Length 271;  
Best Local Similarity 63.6%; Pred. No. 73;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GIEALPRTTHS 11  
Db 114 GLEALPAVHRS 124  
RESULT 9  
AAU63605  
ID AAU63605 standard; protein; 420 AA.  
XX  
XX AC AAU63605;  
XX  
XX 27-FEB-2002 (first entry)  
DT  
XX  
XX Propionibacterium acnes immunogenic protein #24501.  
DE  
XX  
XX SAPHO syndrome; synovitis; acne; pustulosis; hyetosis; osteomyelitis;  
KM uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
XX dermatological; osteopathic; neuroprotectant.  
XX  
XX Propionibacterium acnes.  
OS  
XX  
XX WO200181581-A2.  
XX  
XX 01-NOV-2001.  
XX  
XX 20-APR-2001; 2001WO-US012865.  
XX  
XX 21-APR-2000; 2000US-0199047P.  
PR 02-JUN-2000; 2000US-0208841P.  
XX 07-JUL-2000; 2000US-0216747P.  
XX

PA (CORI-) CORIXA CORP.  
XX  
XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhactia A;  
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
XX  
XX WPI: 2001-616774/71.  
DR N-PSDB; AAS59634.  
XX  
XX Propionibacterium acnes polypeptides and nucleic acids useful for  
PT vaccinating against and diagnosing infections, especially useful for  
PT treating acne vulgaris.  
XX  
XX Claim 3; SEQ ID NO 24800; 1069pp; English.  
XX  
XX Sequences AAU9105-AAU68017 represent Propionibacterium acnes immunogenic  
CC polypeptides. The proteins and their associated DNA sequences are used in  
CC the treatment, prevention and diagnosis of medical conditions caused by  
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
CC P. acnes is also involved in infections of bone, joints and the central  
CC nervous system, however it is particularly involved in the inflammatory  
CC lesions associated with acne vulgaris. A method for detecting the  
CC presence or absence of P. acnes in a patient comprises contacting a  
CC sample with a binding agent that binds to the proteins of the invention  
CC and determining the amount of bound protein in the sample. The  
CC polypeptides may be used as antigens in the production of antibodies  
CC specific for P. acnes proteins. These antibodies can be used to  
CC downregulate expression and activity of P. acnes polypeptides and  
CC therefore treat P. acnes infections. The antibodies may also be used as  
CC diagnostic agents for determining P. acnes presence, for example, by  
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 420 AA;  
SQ  
Query Match 62.9%; Score 39; DB 4; Length 420;  
Best Local Similarity 70.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 3 EALPRTTHSQ 12  
Db 404 KAVPRRHSSQ 413  
RESULT 10  
ABW60124  
ID ABW60124 standard; protein; 420 AA.  
XX  
XX AC ABW60124;  
XX  
XX 20-OCT-2003 (first entry)  
DT  
XX  
XX Propionibacterium acnes membrane-related polypeptide #24800.  
DE  
XX  
XX Acne vulgaris; anti-seborrheic; dermatological; antibacterial;  
KM immunostimulant; immune response; vaccine.  
XX  
XX Propionibacterium acnes.  
OS  
XX  
XX WO2003033515-A1.  
XX  
XX 24-APR-2003.  
XX  
XX 11-OCT-2002; 2002WO-US032727.  
XX  
XX 15-OCT-2001; 2001US-00978825.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Mitcham JL, Skeiky YAM, Persing DH, Bhactia A, Maisonneuve JL;  
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;

PI Barth B, Vallieve-Douglase J;  
 XX WPI; 2003-381789/36.  
 DR N-PSDB; ACF64563.  
 XX  
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the  
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,  
 PT or for stimulating an immune response specific for a P. acnes protein.  
 XX  
 PS Claim 3d; SEQ ID NO 24800; 1481pp; English.  
 XX  
 CC The invention relates to an isolated polynucleotide (ACF6435-ACF64733)  
 CC encoding a Propionibacterium acnes protein. The invention also relates to  
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to  
 CC immunogenic fragments of P. acnes polypeptides. The invention  
 CC additionally encompasses expression vectors and host cells comprising a  
 CC polynucleotide of the invention; antibodies against polypeptides of the  
 CC invention; fusion proteins comprising a polypeptide of the invention; a  
 CC method for stimulating an immune response specific for a P. acnes  
 CC polypeptide and an isolated T cell population comprising T cells prepared  
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,  
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or  
 CC antigen-presenting cells that express the polypeptide); a method and kit  
 CC for detecting or determining the presence or absence of P. acnes in a  
 CC patient; and a method for inhibiting the development of P. acnes in a  
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion  
 CC proteins, T cell populations or antigen-presenting cells that express the  
 CC polypeptides are useful for diagnosing, preventing or treating acne  
 CC vulgaris, or for stimulating an immune response specific for a P. acnes  
 CC protein. The polynucleotides can also be used as probes or primers for  
 CC stimulation of an immune response against P. acnes, or for treating acne,  
 CC and the kit is useful for performing a diagnostic assay. The present  
 CC sequence represents a specifically claimed polypeptide which is predicted  
 CC to be encoded by an ORF (open reading frame) contained within the P.  
 CC acnes polynucleotides of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 420 AA;  
 QY Query Match 62.9%; Score 39; DB 6; Length 420;  
 Beat Local Similarity 70.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Db 3 EALPRTESQ 12  
 404 KAVPRRHSQ 413  
 RESULT 11  
 ADJ37227  
 ID ADJ37227 standard; protein; 948 AA.  
 XX  
 AC ADJ37227;  
 XX  
 DT 22-APR-2004 (first entry)  
 DE Human nucleic-acid associated protein NAAp-16 SEQ ID NO:16.  
 XX  
 XX human; nucleic-acid associated protein; NAAp-16; NAAp; antiparkinsonian;  
 KW neurotrophic; neuroprotective; muscular; neuroleptic; antidiabetic;  
 KW antithyroid; cytosolic; dermatological; antiinflammatory;  
 KW immunosuppressive; antiallergic; nephrotropic; virucide; antibacterial;  
 KW fungicide; antiparasitic; protozoacide; antihelminthic; hepatotropic;  
 KW antitartaric; cardiovascular; gastrointestinal; cancer;  
 KW gene therapy; neurodegenerative disorder; Parkinson's disease;  
 KW Alzheimer's disease; muscular disorder; myotonic dystrophy; catatonla;  
 KW endocrine disorder; diabetes; Grave's disease; cancer; leukaemia;  
 KW cervical cancer; breast cancer; immunological disorder; scleroderma;  
 KW systemic lupus erythematosus; allergy; gastrointestinal disorder;  
 KW Crohn's disease; renal disorder; Goodpasture's syndrome; infection;

KW cardiovascular disorder; atherosclerosis; hepatic diseases; cirrhosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO2004011604-A2.  
 XX  
 PD 05-FEB-2004.  
 XX  
 PP 23-JUL-2003; 2003WO-US023245.  
 XX  
 PR 26-JUL-2002; 2002US-0398907P.  
 PR 30-AUG-2002; 2002US-0407068P.  
 PR 26-SEP-2002; 2002US-0414139P.  
 PR 05-NOV-2002; 2002US-0424094P.  
 PR 17-JAN-2003; 2003US-0440912P.  
 PR 24-JAN-2003; 2003US-0442419P.  
 XX  
 PA (INCY-) INCYTE CORP.  
 XX  
 PI Macon PM, Swarnakar A, Jiang X, Jackson AA, Kable AE, Tang YT;  
 PI Forsythe IJ, Elliott VS, Lee SY, Lee EA, Ison CH, Hafalia AJA;  
 PI Khare R, Margus JP, Becha SD, Bulloch SA, Blake JJ, Gandhi AR;  
 PI Griffin JA, Lee S, Yue H, Yang YG, Sprague WW, Baughn MR, Wang JT;  
 PI Gera M, Gietzen KJ, Nguyen DB, Lu DM;  
 XX  
 DR WPI; 2004-143837/14.  
 DR N-PSDB; ADJ37262.  
 XX  
 PT New nucleic acid-associated proteins (NAAp) polypeptides, useful for  
 PT diagnosing, preventing and treating disorders with abnormal activity of  
 PT NAAp, e.g. neurological, immunological, cardiovascular disorders and  
 PT cancer.  
 PT  
 PS Claim 1; SEQ ID NO 16; 290pp; English.  
 XX  
 CC The present sequence represents a human nucleic-acid associated protein  
 CC designated NAAp-16. NAAp sequences have antiparkinsonian, neurotrophic,  
 CC neuroprotective, muscular, neuroleptic, antidiabetic, antithyroid,  
 CC cytosolic, dermatological, antiinflammatory, immunosuppressive,  
 CC antiallergic, nephrotropic, virucide, antibacterial, fungicide,  
 CC antiparasitic, protozoacide, antihelminthic, antitartaric, cancer,  
 CC cardiovascular, gastrointestinal and hepatotropic activities, and can be  
 CC used in gene therapy. The NAAp polypeptide or its fragments, and the  
 CC polynucleotide encoding the polypeptide are useful in diagnosing,  
 CC preventing, and treating disorders associated with an abnormal expression  
 CC or activity of NAAp (nucleic acid-associated proteins), such as  
 CC neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's  
 CC disease), muscular disorders (e.g. myotonic dystrophy, catatonla),  
 CC endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.  
 CC leukaemia, cervical or breast cancer), immunological disorders (e.g.  
 CC scleroderma, systemic lupus erythematosus, allergies), gastrointestinal  
 CC disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's  
 CC syndrome), infections (e.g. viral, bacterial, fungal, parasitic,  
 CC protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis),  
 CC or hepatic diseases (e.g. cirrhosis). NAAp or its fragments may also be  
 CC used in screening for compounds that specifically bind to and modulate  
 CC the activity of NAAp. The polynucleotides can be used to create humanised  
 CC animals or transgenic animals to model human disease.  
 XX  
 SQ Sequence 948 AA;  
 QY Query Match 62.9%; Score 39; DB 8; Length 948;  
 Beat Local Similarity 72.7%; Pred. No. 2.8e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Db 2 EALPRTESQ 12  
 105 VBALRCHESQ 115  
 RESULT 12  
 ABB11798  
 ID ABB11798 standard; peptide; 509 AA.



```
FT /note= "Encoded by AA codon of the sequence {seqid:1}"
FT Misc-difference 620
FT /note= "Encoded by GTC codon of the sequence {seqid:4}"
FT Misc-difference 705
FT /note= "Encoded by GGC codon of the sequence {seqid:4}"
FT Misc-difference 708
FT /note= "Encoded by AAG codon of the sequence {seqid:1}"
FT Misc-difference 741
FT /note= "Encoded by TT codon of the sequence {seqid:1}"
FT Misc-difference 755
FT /note= "Encoded by GGC codon of the sequence {seqid:4}"
XX
XX US2004102619-A1.
XX
XX 27-MAY-2004.
XX
XX 21-NOV-2002; 2002US-00301015.
XX
XX 21-NOV-2002; 2002US-00301015.
XX
XX (DUNN/) DUNN-COLEMAN N.
XX (WARD/) WARD M.
XX
XX Dunn-Coleman N, Ward M;
XX
XX WPI; 2004-399738/37.
XX N-PSDB; ADP64396, ADP64399, ADP64401.
XX
XX Novel BGL7 polypeptide having beta glucosidase activity useful for
XX improving yeast dough or baked good made from such dough, for preparing
XX detergent compositions or for enhancing potential aroma finished wine
XX product.
XX
XX Claim 18; Fig 2; 25pp; English.
XX
XX The invention relates to beta-glucosidase BGL7 (EC 3.2.1.21) polypeptide
XX and polynucleotide from Trichoderma. The enzyme is useful for improving
XX the characteristics of a yeast dough or baked good made from such dough,
XX for preparing detergent composition, for enhancing the potential aroma of
XX finished wine product, for hydrolysis of cellulose to its sugar
XX components, for preparing cellulase composition for use in detergents or
XX for degradation of biomass into sugar for bio-ethanol production. The
XX present sequence is Trichoderma reesei beta-glucosidase BGL7 precursor
XX protein.
XX
XX Sequence 765 AA;
SQ
XX
XX Query Match 61.3%; Score 38; DB 8; Length 765;
XX Best Local Similarity 50.0%; Pred. No. 3.4e+02;
XX Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 1 GREALPRTTHSQ 12
XX | : | | | |
XX 28 GVSQIPSTHSQ 39
DB
XX
XX RESULT 14
XX ABO70514
XX ID ABO70514 standard; protein; 201 AA.
XX
XX ABO70514;
XX
XX 29-JUL-2004 (first entry)
XX
XX Pseudomonas aeruginosa polypeptide #2689.
XX
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
XX Pseudomonas aeruginosa.
XX
XX US6551795-B1.
XX
XX 22-APR-2003.
PD
```

```
XX
XX 18-FEB-1999; 99US-00252991.
XX
XX 18-FEB-1998; 98US-0074788P.
XX 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
XX WPI; 2003-615309/58.
XX N-PSDB; ABD04085.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostic, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 19260; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABO67826-
XX ABO84336 represent P. aeruginosa polypeptides of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
XX Sequence 201 AA;
SQ
XX
XX Query Match 59.7%; Score 37; DB 7; Length 201;
XX Best Local Similarity 66.7%; Pred. No. 1.3e+02;
XX Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 GREALPRTTH 9
XX | : | | | |
XX 172 GRTLPRTTH 180
DB
XX
XX RESULT 15
XX ABO71665
XX ID ABO71665 standard; protein; 241 AA.
XX
XX ABO71665;
XX
XX 29-JUL-2004 (first entry)
XX
XX Pseudomonas aeruginosa polypeptide #3840.
XX
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
XX Pseudomonas aeruginosa.
XX
XX US6551795-B1.
XX
XX 22-APR-2003.
XX
XX 18-FEB-1999; 99US-00252991.
XX
XX 18-FEB-1998; 98US-0074788P.
XX 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
```

XX WPI: 2003-615309/58.  
DR N-PSDB; ABD05236.  
XX  
PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.  
XX  
PS Disclosure; SEQ ID NO 20411; 455pp; English.  
XX  
CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs, as templates for recombinant production of *P. aeruginosa*-derived peptides or polypeptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused infection, and in detection of *P. aeruginosa* sequences or other sequences of *Pseudomonas* species using biochip technology. Sequences ABO67826-CC ABO64386 represent *P. aeruginosa* polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html  
CC  
XX  
SQ Sequence 241 AA;

Query Match 59.7%; Score 37; DB 7; Length 241;  
Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GIEALPRTHE 10  
Db 141 GIQAARKTHE 150

RESULT 16  
ABBS8234  
ID ABB58234 standard; protein; 307 AA.  
XX  
AC ABB58234;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE *Drosophila melanogaster* polypeptide SEQ ID NO 1494.  
XX  
KW *Drosophila*; developmental biology; cell signalling; insecticide; pharmaceutical.  
XX  
OS *Drosophila melanogaster*.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI: 2001-656860/75.  
DR N-PSDB; ABL02337.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions.  
XX

PS Disclosure; SEQ ID NO 1494; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins (ABBS7737-CC ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
CC  
XX  
SQ Sequence 307 AA;

Query Match 59.7%; Score 37; DB 4; Length 307;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IEALPRTHE 10  
Db 133 LEALPRTHE 141

RESULT 17  
ABO00565  
ID ABO00565 standard; protein; 410 AA.  
XX  
AC ABO00565;  
XX  
DT 06-AUG-2003 (first entry)  
XX  
DE Novel human polypeptide #152.

XX  
KW Human; angiogenesis; cytokine; cell proliferation; pluripotent; cell differentiation; totipotent; stem cell; transplantation; bio-sensor; neuroepithelial cell; autoimmune disease; neural cell; genetic disorder; nerve; brain tissue; central nervous system disease;  
KW peripheral nervous system disease; neuropathy; haematopoiesis; bone; myeloid disorder; lymphoid cell disorder; platelet disorder; tendon; regeneration; cartilage; tendon; ligament; nerve tissue growth; tissue repair; wound healing; burn; ulcer; osteoporosis; cancer; osteoarthritis; bone degenerative disorder; periodontal disease; gut protection; lung fibrosis; liver fibrosis; reperfusion injury;  
KW immune deficiency; infection; autoimmune disorder; allergic reaction; thrombolytic; thrombosis; coagulation disorder; hereditary disorder;  
KW biotechnology; circadian cycle; fertility; metabolism; catabolism; anabolism;  
KW nocturnal; neuroprotective; antiparkinsonian; anticonvulsant;  
KW haemostatic; vulnerary; antiulcer; osteopathic; antiarthritic;  
KW vasotropic; immunostimulant; antibacterial; fungicide; immunosuppressive; antineumatic; antidiabetic; antiashmatic; cytosstatic; virucide.  
XX  
OS Homo sapiens.  
XX  
PN WO2003023013-A2.  
XX  
PD 20-MAR-2003.  
XX  
PF 13-SEP-2002; 2002WO-US029001.  
XX  
PR 13-SEP-2001; 2001US-0322511P.  
PR 12-SEP-2002; 2002US-00243552.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Yang Y, Wang Z, Weng G, Ma Y;  
XX  
DR WPI: 2003-313249/30.  
DR N-PSDB; ACD05642.  
XX  
PT Novel nucleic acids and polypeptides for diagnosis, treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

PT lateral sclerosis.  
 XX Claim 20; SEQ ID NO 488; 300pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human  
 CC polynucleotide sequences and their encoding polypeptides. The novel  
 CC polypeptides exhibit activities relating to angiogenesis, cytokine, cell  
 CC proliferation, cell differentiation, antiinflammatory, and stem cell  
 CC growth factor activities. The polypeptides are involved in the  
 CC proliferation, differentiation and survival of pluripotent and totipotent  
 CC stem cells, and are useful for re-engineering damaged or diseased  
 CC tissues, transplantation, manufacture of bio-pharmaceuticals and  
 CC development of bio-sensors. The polypeptides can be used to manipulate  
 CC stem cells in culture to give rise to neuroepithelial cells that can be  
 CC used to augment or replace cells damaged by illness, autoimmune disease,  
 CC accidental damage or genetic disorders. The polypeptides induce the  
 CC proliferation of neural cells and regeneration of nerve and brain tissue  
 CC and are useful for the treatment of central and peripheral nervous system  
 CC diseases and neuropathies, such as Alzheimer's, Parkinson's disease,  
 CC Huntington's disease, amyotrophic lateral sclerosis (ALS). The  
 CC polypeptides are also involved in chemotactic or chemokinetic activity,  
 CC regulation of hematopoiesis and are useful for treating myeloid or  
 CC lymphoid cell disorders, platelet disorders such as thrombocytopenia and  
 CC for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
 CC growth, in tissue repair, healing of burns, incisions, ulcers, for  
 CC treating osteoporosis, osteoarthritis, bone degenerative disorders, and  
 CC periodontal disease. The polypeptides are also useful for gut protection  
 CC or regeneration and treatment of lung or liver fibrosis, reperfusion  
 CC injury in various tissues, various immune deficiencies and disorders  
 CC including severe combined immunodeficiency (SCID), bacterial or fungal  
 CC infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid  
 CC arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and  
 CC conditions, such as asthma or other respiratory problems. The  
 CC polypeptides are involved in thrombolysis or thrombosis and are useful in  
 CC treatment of various coagulation disorders (including hereditary  
 CC disorders such as haemophilia) or to enhance coagulation and other  
 CC haemostatic events in treating wounds resulting from trauma, surgery or  
 CC other causes. The polypeptides exhibit immune stimulating or immune  
 CC suppressing activity, and are useful for treating autoimmune diseases or  
 CC cancer. They also inhibit the growth, infection or function of infectious  
 CC agents such as bacteria, fungi, viruses, effect biorythms or circadian  
 CC cycles of rhythms, fertility of male or female subjects, metabolism,  
 CC catabolism, and anabolism. AB000414-AB000749 represent the novel  
 CC polypeptides of the invention. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX Sequence 410 AA;  
 SQ  
 Query Match 59.7%; Score 37; DB 6; Length 410;  
 Best Local Similarity 60.0%; Pred. No. 2.7e+02;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IEALPRTSES 11  
 : ||| : |||  
 Db 140 LSAIPRSHSA 149

RESULT 18  
 ID AB064452 standard; protein; 568 AA.  
 XX  
 AC AB064452;  
 XX  
 DT 29-JUN-2004 (first entry)  
 XX  
 DE Klebsiella pneumoniae polypeptide seqid 10969.  
 XX  
 KW Recombinant expression vector; transcription regulatory element;  
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.  
 XX  
 OS Klebsiella pneumoniae.

XX US610836-B1.  
 PN 26-AUG-2003.  
 PD  
 XX 27-JAN-2000; 2000US-00489039.  
 PF  
 XX 29-JAN-1999; 99US-0117747P.  
 PR  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 PA  
 XX Breton GL, Osborne M;  
 PI  
 XX MPI; 2003-895346/82.  
 DR  
 DR N-PSDB; ACH98003.  
 XX  
 PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
 PT preparing a vaccine composition against Klebsiella pneumoniae.  
 PS  
 XX Disclosure; SEQ ID NO 10969; 932pp; English.  
 CC  
 XX The invention describes a new isolated nucleic acid encoding a Klebsiella  
 CC pneumoniae polypeptide. Also described are: a recombinant expression  
 CC vector comprising the nucleic acid, operably linked to a transcription  
 CC regulatory element; and a cell comprising the recombinant expression  
 CC vector. The nucleic acid is useful for preparing a vaccine composition  
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
 CC Klebsiella pneumoniae polypeptide of the invention  
 CC  
 XX Sequence 568 AA;  
 SQ  
 Query Match 59.7%; Score 37; DB 7; Length 568;  
 Best Local Similarity 58.3%; Pred. No. 3.8e+02;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTSESQ 12  
 : ||| : ||| : |||  
 Db 422 GIEVRRRLHQSG 433

RESULT 19  
 ID ABP41544 standard; protein; 126 AA.  
 XX  
 AC ABP41544;  
 XX  
 DT 22-AUG-2002 (first entry)  
 XX  
 DE Human ovarian antigen HCOFQ3, SEQ ID NO:2676.  
 XX  
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200677-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 07-JUN-2001; 2001WO-US018569.  
 XX  
 PR 07-JUN-2000; 2000US-0209467P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX

PI Birse CE, Rosen CA;  
 XX  
 DR WPI: 2002-147876/19.  
 DR N-P5DB: ABQ54621.  
 XX  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
 PT cancer), immune disorders, cardiovascular disorders and neurological  
 PT diseases.  
 XX  
 PS Claim 11; SEQ ID NO 2676; 2922pp; English.  
 XX  
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX  
 SQ Sequence 126 AA;  
 XX  
 QY  
 Db 1 GIALPRTHEO 12  
 | : : : : |  
 102 GVPSIPQTHSPQ 113  
 Query Match 58.1%; Score 36; DB 5; Length 126;  
 Best Local Similarity 41.7%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

RESULT 20  
 ABM69852  
 ID ABM69852 standard; protein; 152 AA.  
 XX  
 AC ABM69852;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Photorhabdus luminescens protein sequence #2949.  
 XX  
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
 KW detection; food; gene expression; plant; animal; microorganism; toxin;  
 KW antibiotic; biopesticide; virulence factor; disease model; plague;  
 KW whooping cough.  
 XX  
 OS Photorhabdus luminescens.  
 XX  
 PN WO200294867-A2.  
 XX  
 PD 28-NOV-2002.

XX  
 PF 07-FEB-2002; 2002WO-IB003040.  
 XX  
 PR 07-FEB-2001; 2001FR-00001659.  
 XX  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Duchaud E, Taourit S, Glaeser P, Frangeul L, Kunet F, Danchin A;  
 PI Buchrieser C;  
 XX  
 DR WPI: 2003-148459/14.  
 XX  
 PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
 XX  
 PS Claim 2; SEQ ID NO 2949; 1205pp; French.  
 XX  
 CC The invention relates to the isolation of genes and their encoded  
 CC proteins from Photorhabdus luminescens. The isolated sequences are  
 CC sources of probes and primers for detecting the genome of P. luminescens  
 CC and related species; to study polymorphisms; for gene analysis and for  
 CC detection/amplification of the genes. Antibodies (Ab) raised against the  
 CC polypeptides encoded by the genes are used for detection/identification  
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
 CC carry a gene-containing vector are used to select compounds that  
 CC modulate, regulate, induce or inhibit expression of the genes in plants,  
 CC animals or microorganisms other than P. luminescens and are able to alter  
 CC response or sensitivity to toxins and antibiotics produced by P.  
 CC luminescens. Cells transformed to express the genes are useful for  
 CC recombinant production of the proteins, particularly toxins and  
 CC antibiotics useful as insecticides, bactericides and fungicides. The  
 CC genes, proteins, vectors containing the genes and Ab are also useful  
 CC therapeutically (to treat microbial infection by bacteria or fungi that  
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
 CC biopesticides. Other uses of the genes and the proteins are as virulence  
 CC factors and for identifying targets of human diseases for which P.  
 CC luminescens is a model (particularly plague and whooping cough). This  
 CC sequence represents one of the isolated P. luminescens proteins  
 CC  
 XX  
 SQ Sequence 152 AA;  
 XX  
 QY  
 Db 3 EALPRTHEO 11  
 | | | | |  
 96 EALPRTHEA 104  
 Query Match 58.1%; Score 36; DB 6; Length 152;  
 Best Local Similarity 77.8%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 21  
 ABM69781  
 ID ABM69781 standard; protein; 152 AA.  
 XX  
 AC ABM69781;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Photorhabdus luminescens protein sequence #2878.  
 XX  
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
 KW detection; food; gene expression; plant; animal; microorganism; toxin;  
 KW antibiotic; biopesticide; virulence factor; disease model; plague;  
 KW whooping cough.  
 XX  
 OS Photorhabdus luminescens.  
 XX  
 PN WO200294867-A2.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 07-FEB-2002; 2002WO-IB003040.

XX 07-FEB-2001; 2001FR-00001659.  
PR (INSP ) INST PASTEUR.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
PA  
XX  
PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A,  
FI Buchrieser C;  
DR WPI; 2003-148459/14.  
XX  
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
XX  
PS Claim 2; SEQ ID NO 2878; 1205bp; French.  
XX  
CC The invention relates to the isolation of genes and their encoded  
CC proteins from Photorhabdus luminescens. The isolated sequences are  
CC sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins  
XX  
SQ Sequence 152 AA;  
XX  
Query Match 58.1%; Score 36; DB 6; Length 152;  
Best Local Similarity 77.8%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 EALPRTRES 11  
||| |||:  
Db 96 EALKRTTREA 104  
XX  
RESULT 22  
ADK16367  
ID ADK16367 standard; protein; 179 AA.  
XX  
AC ADK16367;  
XX  
DT 06-MAY-2004 (first entry)  
DE Nanoarchaeum equitans cancer-associated (CA) protein #159.  
XX  
KM cancer-associated gene; CA gene; cancer; carcinoma; lymphoma; leukaemia.  
XX Nanoarchaeum equitans.  
OS  
PN WO2003093434-A2.  
XX  
PD 13-NOV-2003.  
XX  
PF 01-MAY-2003; 2003WO-US013699.  
XX  
PR 01-MAY-2002; 2002US-037447P.  
XX  
PA (DIVE-) DIVERSA CORP.  
XX

PI Stetter KO, Waters E, Kretz K, Podar M, Richardson T;  
PI Noordewier M;  
XX  
XX WPI; 2004-053041/05.  
DR N-PSDB; ADK16366.  
XX  
XX  
PT New recombinant cancer-associated genes, such as KCNU9, useful for  
PT diagnosing or treating carcinoma, e.g. breast, colon, rectal, pancreatic,  
PT cervical, or skin cancers, lymphomas, or leukemia.  
XX  
XX  
PS Claim 64; SEQ ID NO 319; 251bp; English.  
XX  
XX  
CC The invention comprises then amino acid and coding sequences of cancer-  
CC associated (CA) genes isolated from Nanoarchaeum equitans. The invention  
CC also comprises the Nanoarchaeum equitans genome. The DNA and protein  
CC sequences of the invention are useful for diagnosing and treating cancer  
CC (e.g. carcinoma, lymphoma, or leukaemia). The present amino acid sequence  
CC represents a Nanoarchaeum equitans CA protein of the invention.  
XX  
SQ Sequence 179 AA;  
XX  
Query Match 58.1%; Score 36; DB 8; Length 179;  
Best Local Similarity 45.5%; Pred. No. 1.7e+02;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 2 IEALPRTRESQ 12  
:| |||:|:  
Db 91 LELGPKTHKGS 101  
XX  
RESULT 23  
AAM40723  
ID AAM40723 standard; protein; 198 AA.  
XX  
XX AAM40723;  
AC  
XX  
DT 22-OCT-2001 (first entry)  
DE  
XX  
DE Human polypeptide SEQ ID NO 5654.  
XX  
XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;  
XX peripheral nervous system; neuropathy; central nervous system; CNS;  
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;  
XX leukaemia.  
OS  
XX Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
XX 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YF, Liu C, Agundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou F, Goodrich R, Drmanac RT;  
XX  
DR WPI; 2001-442253/47.  
DR N-PSDB; AAI59879.

XX Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
XX Example 2; SEQ ID NO 5654; 10078bp; English.  
XX  
XX The invention relates to human nucleic acids (AA157798-AA161369) and the  
CC encoded polypeptides (AA038642-AA042213) with neurotropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localized neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilization of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 198 AA;  
  
Query Match 58.1%; Score 36; DB 4; Length 198;  
Best Local Similarity 58.3%; Pred. No. 1.9e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 GIEALPRTHEQ 12  
||: ||| |||  
Db 128 GIDRPRRLHRSQ 139  
  
RESULT 24  
ABO72967  
ID ABO72967 standard; protein; 251 AA.  
XX  
XX ABO72967;  
AC  
XX 29-JUN-2004 (first entry)  
DT  
XX Pseudomonas aeruginosa polypeptide #5142.  
DE  
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
KM  
XX Pseudomonas aeruginosa.  
OS  
XX US6551795-B1.  
PN  
XX 22-APR-2003.  
PD  
XX 18-FEB-1999; 99US-00252991.  
PF  
XX 18-FEB-1998; 98US-0074788P.  
PR  
XX 27-JUL-1998; 98US-0094190P.  
PS  
XX (GENO-) GENOME THERAPEUTICS CORP.  
PA  
XX  
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX WPI; 2003-615309/58.  
DR N-PSDB; ABD06538.  
XX  
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX  
XX Disclosure; SEQ ID NO 21713; 455bp; English.  
XX  
XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a

CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 251 AA;  
  
Query Match 58.1%; Score 36; DB 7; Length 251;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 IEALPRTHE 10  
: || ||| |||  
Db 20 VEQAPRTHE 28  
  
RESULT 25  
ABU21788  
ID ABU21788 standard; protein; 336 AA.  
XX  
XX ABU21788;  
AC  
XX 19-JUN-2003 (first entry)  
DT  
XX Protein encoded by Prokaryotic essential gene #7315.  
DE  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
KM  
XX Burkholderia fungorum.  
OS  
XX WO200277183-A2.  
PN  
XX 03-OCT-2002.  
PD  
XX 21-MAR-2002; 2002WO-US009107.  
PF  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948893.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
PA  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA25658.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 25; SEQ ID NO 49712; 1766bp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular





CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. Improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 403 AA:  
 Query Match 58.1%; Score 36; DB 8; Length 403;  
 Best Local Similarity 70.0%; Pred. NO. 4.1e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEALPRTHES 11  
 DB 130 ITGLPRNHES 139

RESULT 30  
 ADS26083 ID ADS26083 standard; protein; 403 AA.  
 XX  
 AC ADS26083;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Bacterial polypeptide #15116.  
 XX  
 KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.  
 XX  
 OS Bacteria.  
 XX  
 FN US2003233675-A1.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 20-FEB-2003; 2003US-00369493.  
 XX  
 PR 21-FEB-2002; 2002US-0360039P.  
 XX  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE S J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 PI Cao Y, Hinkle SJ, Slater SC, Chen X, Goldman BS;  
 XX  
 DR WPI, 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.  
 PT  
 PT  
 PS Claim 1; SEQ ID NO 15116; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. Improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 403 AA:

Query Match 58.1%; Score 36; DB 8; Length 403;  
 Best Local Similarity 70.0%; Pred. NO. 4.1e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEALPRTHES 11  
 DB 130 ITGLPRNHES 139

Search completed: August 1, 2005, 08:45:20  
 Job time : 172 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using SW model

Run on: August 1, 2005, 08:48:30 ; Search time 155 Seconds

(Without alignments)  
30.163 Million cell updates/sec

Title: US-10-663-749-18

Perfect score: 62

Sequence: 1 GIEALPRTHEGQ 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	12	US-10-663-749-18	Sequence 18, Appl
2	62	100.0	14	US-10-663-749-20	Sequence 20, Appl
3	62	100.0	237	US-10-608-536-11	Sequence 11, Appl
4	62	100.0	237	US-10-663-749-11	Sequence 11, Appl
5	62	100.0	500	US-10-236-031B-34	Sequence 34, Appl
6	62	100.0	500	US-10-608-536-15	Sequence 15, Appl
7	62	100.0	500	US-10-663-749-15	Sequence 15, Appl
8	62	100.0	500	US-10-923-348-2	Sequence 2, Appl
9	41	66.1	12	US-10-663-749-19	Sequence 19, Appl
10	40	64.5	360	US-10-425-115-274140	Sequence 274140, Appl
11	40	64.5	924	US-10-739-930-6590	Sequence 6590, Appl

12	38	61.3	61	US-10-424-599-269929	Sequence 269929, Appl
13	38	61.3	117	US-10-425-115-222869	Sequence 222869, Appl
14	38	61.3	161	US-10-425-115-342271	Sequence 342271, Appl
15	38	61.3	179	US-10-425-115-286760	Sequence 286760, Appl
16	38	61.3	509	US-10-276-774-2168	Sequence 2168, Appl
17	38	61.3	765	US-10-301-015-2	Sequence 2, Appl
18	37	59.7	69	US-10-425-115-269133	Sequence 269133, Appl
19	37	59.7	410	US-10-243-552-573	Sequence 573, Appl
20	37	58.1	101	US-10-437-963-110387	Sequence 110387, Appl
21	36	58.1	105	US-10-425-115-191562	Sequence 191562, Appl
22	36	58.1	126	US-10-264-049-2676	Sequence 2676, Appl
23	36	58.1	141	US-10-425-114-68790	Sequence 68790, Appl
24	36	58.1	150	US-10-425-115-303972	Sequence 303972, Appl
25	36	58.1	336	US-10-282-122A-49712	Sequence 49712, Appl
26	36	58.1	398	US-10-739-930-7940	Sequence 7940, Appl
27	36	58.1	403	US-10-369-493-11658	Sequence 11658, Appl
28	36	58.1	403	US-10-369-493-14548	Sequence 14548, Appl
29	36	58.1	403	US-10-369-493-15116	Sequence 15116, Appl
30	36	58.1	423	US-10-425-115-269700	Sequence 269700, Appl
31	36	58.1	424	US-10-437-963-141677	Sequence 141677, Appl
32	36	58.1	449	US-10-767-701-46347	Sequence 46347, Appl
33	36	58.1	507	US-09-910-087-19	Sequence 19, Appl
34	36	58.1	509	US-09-910-087-21	Sequence 21, Appl
35	36	58.1	509	US-10-437-963-110395	Sequence 110395, Appl
36	36	58.1	509	US-10-723-860-2484	Sequence 2484, Appl
37	36	58.1	509	US-10-156-761-110060	Sequence 110060, Appl
38	36	58.1	738	US-10-437-963-110386	Sequence 110386, Appl
39	36	58.1	865	US-10-437-963-176404	Sequence 176404, Appl
40	36	58.1	1028	US-10-314-657-24	Sequence 24, Appl
41	36	58.1	1134	US-10-473-193-24	Sequence 24, Appl
42	36	58.1	1251	US-10-437-963-160953	Sequence 160953, Appl
43	36	58.1	1530	US-10-087-192-300	Sequence 300, Appl
44	36	58.1	1790	US-10-437-963-143861	Sequence 143861, Appl
45	35	56.5	27	US-10-097-876-290	Sequence 290, Appl
46	35	56.5	67	US-10-425-115-345469	Sequence 290, Appl
47	35	56.5	103	US-10-425-115-311812	Sequence 311812, Appl
48	35	56.5	123	US-10-425-115-231403	Sequence 231403, Appl
49	35	56.5	149	US-10-282-122A-49857	Sequence 49857, Appl
50	35	56.5	169	US-10-437-963-124765	Sequence 124765, Appl
51	35	56.5	214	US-10-425-115-255326	Sequence 255326, Appl
52	35	56.5	244	US-10-369-493-13007	Sequence 13007, Appl
53	35	56.5	257	US-10-767-701-37016	Sequence 37016, Appl
54	35	56.5	258	US-10-425-115-238102	Sequence 238102, Appl
55	35	56.5	275	US-10-425-114-52283	Sequence 52283, Appl
56	35	56.5	329	US-10-425-115-357563	Sequence 357563, Appl
57	35	56.5	439	US-10-437-963-180843	Sequence 180843, Appl
58	35	56.5	439	US-10-097-876-283	Sequence 283, Appl
59	35	56.5	439	US-10-372-876-283	Sequence 283, Appl
60	35	56.5	440	US-10-424-599-198538	Sequence 198538, Appl
61	35	56.5	456	US-10-732-823-3008	Sequence 3008, Appl
62	35	56.5	470	US-10-369-493-16985	Sequence 16985, Appl
63	35	56.5	505	US-10-437-963-124766	Sequence 124766, Appl
64	35	56.5	509	US-10-437-963-128983	Sequence 128983, Appl
65	35	56.5	555	US-10-104-047-2530	Sequence 2530, Appl
66	35	56.5	555	US-10-425-115-298951	Sequence 298951, Appl
67	35	56.5	592	US-10-425-114-38308	Sequence 38308, Appl
68	35	56.5	598	US-10-369-493-4091	Sequence 4091, Appl
69	35	56.5	628	US-10-437-963-128980	Sequence 128980, Appl
70	35	56.5	691	US-10-739-930-7223	Sequence 7223, Appl
71	35	56.5	703	US-10-282-122A-51965	Sequence 51965, Appl
72	35	56.5	812	US-10-437-963-192780	Sequence 192780, Appl
73	35	56.5	1274	US-09-746-481-12	Sequence 12, Appl
74	35	56.5	1615	US-10-443-710-108	Sequence 108, Appl
75	35	56.5	55	US-09-864-408A-6202	Sequence 6202, Appl
76	34	54.8	67	US-09-864-761-48290	Sequence 48290, Appl
77	34	54.8	99	US-10-425-115-331629	Sequence 331629, Appl
78	34	54.8	69	US-10-767-701-33288	Sequence 33288, Appl
79	34	54.8	71	US-09-864-408A-3028	Sequence 3028, Appl
80	34	54.8	91	US-10-425-115-226778	Sequence 226778, Appl
81	34	54.8	100	US-09-864-408A-33234	Sequence 33234, Appl
82	34	54.8	128	US-10-767-701-40805	Sequence 40805, Appl
83	34	54.8	154	US-10-767-701-32836	Sequence 32836, Appl
84	34	54.8	16	US-10-767-701-32836	Sequence 32836, Appl

85	34	54.8	158	16	US-10-425-115-285555	Sequence 285555,
86	34	54.8	159	16	US-10-425-115-262461	Sequence 262461,
87	34	54.8	160	16	US-10-767-701-36069	Sequence 36069, A
88	34	54.8	263	14	US-10-128-714-3028	Sequence 3028, Ap
89	34	54.8	301	16	US-10-425-115-249295	Sequence 249295,
90	34	54.8	303	15	US-10-282-122A-71719	Sequence 71719, A
91	34	54.8	313	14	US-10-128-714-8028	Sequence 8028, Ap
92	34	54.8	334	15	US-10-369-493-15984	Sequence 15984, A
93	34	54.8	334	15	US-10-369-493-16342	Sequence 16342, A
94	34	54.8	340	15	US-10-369-493-15609	Sequence 15609, A
95	34	54.8	340	15	US-10-289-762-362	Sequence 362, App
96	34	54.8	341	15	US-10-424-599-175916	Sequence 175916,
97	34	54.8	350	15	US-10-425-114-46691	Sequence 46691, A
98	34	54.8	363	16	US-10-437-963-167680	Sequence 167680,
99	34	54.8	363	17	US-10-814-850-3	Sequence 3, Appl1
100	34	54.8	377	17	US-10-814-850-10	Sequence 10, Appl1
101	34	54.8	409	15	US-10-282-122A-51298	Sequence 51298, A
102	34	54.8	421	15	US-10-282-122A-61590	Sequence 61590, A
103	34	54.8	477	15	US-10-425-114-71233	Sequence 71233, A
104	34	54.8	604	14	US-10-319-799-14	Sequence 14, Appl1
105	34	54.8	628	15	US-10-369-493-13998	Sequence 13998, A
106	34	54.8	631	16	US-10-437-963-110431	Sequence 110431,
107	34	54.8	637	17	US-10-505-486-101	Sequence 101, App
108	34	54.8	648	16	US-10-437-963-110466	Sequence 110466,
109	34	54.8	922	16	US-10-437-963-137943	Sequence 137943,
110	34	54.8	962	16	US-10-437-963-157765	Sequence 157765,
111	34	54.8	1046	17	US-10-493-759-24	Sequence 24, Appl1
112	34	54.8	1088	14	US-10-390-303-3	Sequence 3, Appl1
113	34	54.8	1088	14	US-10-380-303-4	Sequence 4, Appl1
114	34	54.8	1088	15	US-10-284-130-4	Sequence 4, Appl1
115	34	54.8	1373	18	US-10-840-512-180	Sequence 180, App
116	34	54.8	1461	16	US-10-437-963-110037	Sequence 110037,
117	34	54.8	5125	16	US-10-437-963-107204	Sequence 107204,
118	34	54.0	625	17	US-10-732-923-22726	Sequence 22726, A
33	5	53.2	31	9	US-09-864-761-40538	Sequence 40538, A
119	33	53.2	47	16	US-10-425-115-295766	Sequence 295766,
120	33	53.2	48	16	US-10-425-115-239149	Sequence 239149,
121	33	53.2	55	14	US-10-194-746-7	Sequence 7, Appl1
122	33	53.2	70	16	US-10-425-115-333369	Sequence 333369,
123	33	53.2	87	16	US-10-767-701-59451	Sequence 59451, A
124	33	53.2	90	15	US-10-425-114-55039	Sequence 55039, A
125	33	53.2	93	15	US-10-424-599-191580	Sequence 191580,
126	33	53.2	94	15	US-10-424-599-276389	Sequence 276389,
127	33	53.2	99	16	US-10-424-599-179792	Sequence 179792,
128	33	53.2	102	10	US-09-764-891-4010	Sequence 4010, Ap
129	33	53.2	104	16	US-10-425-115-285098	Sequence 285098,
130	33	53.2	108	16	US-10-425-115-360794	Sequence 360794,
131	33	53.2	118	9	US-10-084-846A-26	Sequence 26, Appl1
132	33	53.2	118	9	US-09-771-161A-97	Sequence 97, Appl1
133	33	53.2	118	16	US-10-425-115-250752	Sequence 250752,
134	33	53.2	134	16	US-10-767-701-44026	Sequence 44026, A
135	33	53.2	141	15	US-10-425-114-49582	Sequence 49582, A
136	33	53.2	147	16	US-10-425-114-57912	Sequence 57912, A
137	33	53.2	148	16	US-10-767-701-57912	Sequence 57912, A
138	33	53.2	162	14	US-10-067-443-18	Sequence 18, Appl1
139	33	53.2	162	14	US-10-067-443-18	Sequence 18, Appl1
140	33	53.2	162	15	US-10-649-773-18	Sequence 18, Appl1
141	33	53.2	163	16	US-10-651-722-18	Sequence 18, Appl1
142	33	53.2	175	15	US-10-424-599-145339	Sequence 145339,
143	33	53.2	175	15	US-10-424-599-145339	Sequence 145339,
144	33	53.2	179	15	US-10-424-599-207612	Sequence 207612,
145	33	53.2	179	15	US-10-425-114-37863	Sequence 37863, A
146	33	53.2	189	15	US-10-425-114-67724	Sequence 67724, A
147	33	53.2	203	15	US-10-094-749-2410	Sequence 2410, Ap
148	33	53.2	203	15	US-10-424-599-17696	Sequence 17696, A
149	33	53.2	206	16	US-10-767-701-35999	Sequence 35999, A
150	33	53.2	250	18	US-10-784-592-38	Sequence 38, Appl1

## ALIGNMENTS

```
Sequence 18, Application US/10663749
; Publication No. US20040092722A1
; GENERAL INFORMATION:
; APPLICANT: TANABE, TADASHI
; APPLICANT: YOKOYAMA, CHIEKO
; TITLE OF INVENTION: ANTIBODIES SPECIFIC TO HUMAN PROSTACYCLIN SYNTHASE
; FILE REFERENCE: Q76409
; CURRENT FILING DATE: US/10/663, 749
; PRIOR APPLICATION NUMBER: 09/670,582
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: 09/037,758
; PRIOR FILING DATE: 1998-01-10
; PRIOR APPLICATION NUMBER: 08/578,706
; PRIOR FILING DATE: 1995-12-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-663-749-18

Query Match          100.0%; Score 62; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GIEALPRTTHSQ 12
|||||
Db      1 GIEALPRTTHSQ 12
```

```
RESULT 2
US-10-663-749-20
; Sequence 20, Application US/10663749
; Publication No. US20040092722A1
; GENERAL INFORMATION:
; APPLICANT: TANABE, TADASHI
; APPLICANT: YOKOYAMA, CHIEKO
; TITLE OF INVENTION: ANTIBODIES SPECIFIC TO HUMAN PROSTACYCLIN SYNTHASE
; FILE REFERENCE: Q76409
; CURRENT FILING DATE: US/10/663, 749
; PRIOR APPLICATION NUMBER: 09/670,582
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: 09/037,758
; PRIOR FILING DATE: 1998-01-10
; PRIOR APPLICATION NUMBER: 08/578,706
; PRIOR FILING DATE: 1995-12-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-663-749-20
```

```
Query Match          100.0%; Score 62; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GIEALPRTTHSQ 12
|||||
Db      3 GIEALPRTTHSQ 14
```

US-10-608-536-11  
; Sequence 11, Application US/10608536  
; Publication No. US20040049015A1  
; GENERAL INFORMATION:  
; APPLICANT: TANABE, Tadashi  
; TITLE OF INVENTION: PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/608,536  
; FILING DATE: 30-Jun-2003  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,709  
; FILING DATE: 28-DEC-1995  
; APPLICATION NUMBER: PCT/JP95/00838  
; FILING DATE: 27-APR-1995  
; APPLICATION NUMBER: JP 114316/1994  
; FILING DATE: 28-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gubinsky, Louis  
; REGISTRATION NUMBER: 24,835  
; REFERENCE/DOCKET NUMBER: Q40439  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)293-7860  
; TELEFAX: (202)293-7860  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 237 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-608-536-11  
Query Match 100.0%; Score 62; DB 15; Length 237;  
Best Local Similarity 100.0%; Pred. No. 0.0052;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GIEALPRTHEQ 12  
|||  
Db 182 GIEALPRTHEQ 193  
RESULT 4  
US-10-663-749-11  
; Sequence 11, Application US/10663749  
; Publication No. US20040092722A1  
; GENERAL INFORMATION:  
; APPLICANT: TANABE, Tadashi  
; APPLICANT: YOKOYAMA, CHIKO  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC TO HUMAN PROSTACYCLIN SYNTHASE  
; FILE REFERENCE: Q76409  
; CURRENT APPLICATION NUMBER: US/10/663,749  
; PRIOR APPLICATION NUMBER: 2003-09-17  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 09/037,758  
; PRIOR FILING DATE: 1998-01-10  
; PRIOR APPLICATION NUMBER: 08/578,706  
; PRIOR FILING DATE: 1995-12-28  
; NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-663-749-11  
Query Match 100.0%; Score 62; DB 15; Length 237;  
Best Local Similarity 100.0%; Pred. No. 0.0052;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GIEALPRTHEQ 12  
|||  
Db 182 GIEALPRTHEQ 193  
RESULT 5  
US-10-236-031B-34  
; Sequence 34, Application US/10236031B  
; Publication No. US20030219760A1  
; GENERAL INFORMATION:  
; APPLICANT: Gordon, Gavin J.  
; APPLICANT: Jensen, Rodrick V.  
; APPLICANT: Guillans, Steven R.  
; APPLICANT: Bueno, Raphael  
; TITLE OF INVENTION: Diagnostic and Prognostic Tests  
; FILE REFERENCE: B00801/70265 (JRV/JAV)  
; CURRENT APPLICATION NUMBER: US/10/236,031B  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/317,389  
; PRIOR FILING DATE: 2001-09-05  
; PRIOR APPLICATION NUMBER: US 60/407,431  
; PRIOR FILING DATE: 2002-08-30  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 34  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-236-031B-34  
Query Match 100.0%; Score 62; DB 15; Length 500;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GIEALPRTHEQ 12  
|||  
Db 182 GIEALPRTHEQ 193  
RESULT 6  
US-10-608-536-15  
; Sequence 15, Application US/10608536  
; Publication No. US20040049015A1  
; GENERAL INFORMATION:  
; APPLICANT: TANABE, Tadashi  
; TITLE OF INVENTION: PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/608,536  
; FILING DATE: 30-Jun-2003

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/578,709  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: PCT/JP95/00838  
FILING DATE: 27-APR-1995  
APPLICATION NUMBER: JP 114316/1994  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Gubinsky, Louis  
REGISTRATION NUMBER: 24,835  
REFERENCE/DOCKET NUMBER: Q40439  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 500 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-608-536-15

Query Match 100.0%; Score 62; DB 15; Length 500;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIEALPRTHEQ 12  
Db 182 GIEALPRTHEQ 193

RESULT 7  
US-10-663-749-15  
Sequence 15, Application US/10663749  
Publication No. US20040092722A1  
GENERAL INFORMATION:  
APPLICANT: TANABE, TADASHI  
APPLICANT: YOKOYAMA, CHIEKO  
TITLE OF INVENTION: ANTIBODIES SPECIFIC TO HUMAN PROSTACYCLIN SYNTHASE  
FILE REFERENCE: Q76409  
CURRENT APPLICATION NUMBER: US/10/663,749  
CURRENT FILING DATE: 2003-09-17  
PRIOR APPLICATION NUMBER: 09/670,582  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 09/037,758  
PRIOR FILING DATE: 1998-01-10  
PRIOR APPLICATION NUMBER: 08/578,706  
PRIOR FILING DATE: 1995-12-28  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 500  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-663-749-15

Query Match 100.0%; Score 62; DB 15; Length 500;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIEALPRTHEQ 12  
Db 182 GIEALPRTHEQ 193

RESULT 8  
US-10-923-348-2  
Sequence 2, Application US/10923348  
Publication No. US20050080140A1  
GENERAL INFORMATION:  
APPLICANT: Hatase, Toshitsa

APPLICANT: Yokoyama, Chieko  
APPLICANT: Tanabe, Tadashi  
APPLICANT: Angeles Mg, Inc.  
TITLE OF INVENTION: Method for Treating or Preventing Inflammatory Disorders  
FILE REFERENCE: 082399-000100US  
CURRENT APPLICATION NUMBER: US/10/923,348  
CURRENT FILING DATE: 2004-08-20  
PRIOR APPLICATION NUMBER: 06/511,003  
PRIOR FILING DATE: 2003-10-13  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 500  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-923-348-2

Query Match 100.0%; Score 62; DB 17; Length 500;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIEALPRTHEQ 12  
Db 182 GIEALPRTHEQ 193

RESULT 9  
US-10-663-749-19  
Sequence 19, Application US/10663749  
Publication No. US20040092722A1  
GENERAL INFORMATION:  
APPLICANT: TANABE, TADASHI  
APPLICANT: YOKOYAMA, CHIEKO  
TITLE OF INVENTION: ANTIBODIES SPECIFIC TO HUMAN PROSTACYCLIN SYNTHASE  
FILE REFERENCE: Q76409  
CURRENT APPLICATION NUMBER: US/10/663,749  
CURRENT FILING DATE: 2003-09-17  
PRIOR APPLICATION NUMBER: 09/670,582  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 09/037,758  
PRIOR FILING DATE: 1998-01-10  
PRIOR APPLICATION NUMBER: 08/578,706  
PRIOR FILING DATE: 1995-12-28  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Bos sp.  
US-10-663-749-19

Query Match 66.1%; Score 41; DB 15; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.4;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTHEQ 12  
Db 1 GIEALPRTHEQ 12

RESULT 10  
US-10-425-115-274140  
Sequence 274140, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 274140

LENGTH: 360

TYPE: PRT

ORGANISM: Zea mays

FEATURE: Zea mays  
OTHER INFORMATION: Clone ID: MRT4577\_181603C.1.pep  
US-10-425-115-274140

Query Match  
Best Local Similarity 64.5%; Score 40; DB 16; Length 360;  
Pred. No. 81;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1EALPRTHE 9

DB 272 G1EALPRTHE 280

RESULT 11  
US-10-739-930-6590

Sequence 6590, Application US/10739930  
Publication No. US20040216190A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

TITLE OF INVENTION: NOCLETIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

FILE REFERENCE: 38-21(53377)B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 6590

LENGTH: 924

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE: Arabidopsis thaliana  
OTHER INFORMATION: Clone ID: ARATH-23APR03-CS208\_1.p

US-10-739-930-6590

Query Match  
Best Local Similarity 64.5%; Score 40; DB 16; Length 924;  
Pred. No. 2,2e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1EALPRTHE 10

DB 118 G1EALPRTHE 127

RESULT 12  
US-10-424-599-269929

Sequence 269929, Application US/10424599  
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 269929

LENGTH: 61

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT3847\_85766C.1.pep  
US-10-424-599-269929

Query Match  
Best Local Similarity 61.3%; Score 38; DB 15; Length 61;  
Pred. No. 28;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALPRTHE 10

DB 35 ALPRTHE 41

RESULT 13  
US-10-425-115-222869

Sequence 222869, Application US/10425115  
Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 222869

LENGTH: 117

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577\_134847C.1.pep  
US-10-425-115-222869

Query Match  
Best Local Similarity 61.3%; Score 38; DB 16; Length 117;  
Pred. No. 57;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEALPRTHE 11

DB 92 LEALPRTHE 101

RESULT 14  
US-10-425-115-342271

Sequence 342271, Application US/10425115  
Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 342271

LENGTH: 161

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

NAME/KEY: unsure

LOCATION: (1) (161)

OTHER INFORMATION: unsure at all Xaa locations

OTHER INFORMATION:

OTHER INFORMATION: Clone ID: MRT4577\_75314C.1.pep  
US-10-425-115-342271

Query Match  
Best Local Similarity 61.3%; Score 38; DB 16; Length 161;  
Pred. No. 80;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 G1EALPRTHE 12

DB 113 G1EALPRTHE 124

```
RESULT 15
US-10-425-115-286760
; Sequence 286760, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286760
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_2461C.1.pep
US-10-425-115-286760

Query Match          61.3%; Score 38; DB 16; Length 179;
Best Local Similarity 60.0%; Pred. No. 89;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 IEALPRTSES 11
Db      93 LEAIPRSHNS 102

RESULT 16
US-10-276-774-2168
; Sequence 2168, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2168
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2168

Query Match          61.3%; Score 38; DB 15; Length 509;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 GIEALPRTHE 10
Db      390 GVGQIPRVHE 399

RESULT 17
US-10-301-015-2
; Sequence 2, Application US/10301015
; Publication No. US20040102619A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Ward, Michael
```

```
; TITLE OF INVENTION: BGL7 Beta-Glucosidase and Nucleic Acids
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: GC780
; CURRENT APPLICATION NUMBER: US/10/301,015
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-10-301-015-2

Query Match          61.3%; Score 38; DB 16; Length 765;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 GIEALPRTSESQ 12
Db      28 GVSQIPSTHSSQ 39

RESULT 18
US-10-425-115-269133
; Sequence 269133, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 269133
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177047C.1.pep
US-10-425-115-269133

Query Match          59.7%; Score 37; DB 16; Length 69;
Best Local Similarity 54.5%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 GIEALPRTSES 11
Db      50 GFKGFPRTHKS 60

RESULT 19
US-10-243-552-573
; Sequence 573, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y, Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Ma, Yungding
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 807A
; CURRENT APPLICATION NUMBER: US/10/243,552
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,511
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
```

```

; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 998
; SOFTWARE: pf_fl_genes Version 5.0
; SEQ ID NO 573
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-243-552-573

Query Match
Best Local Similarity 59.7%; Score 37; DB 15; Length 410;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IEALPRTSES 11
DB 140 LSLALPSHEA 149

RESULT 20
US-10-437-963-110387
; Sequence 110387, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 110387
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14456C.1.pap
; US-10-437-963-110387

Query Match
Best Local Similarity 58.1%; Score 36; DB 16; Length 101;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIEALPRTSES 11
DB 2 GVFLPKTHQS 12

RESULT 21
US-10-425-115-191562
; Sequence 191562, Application US/10425115

; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 191562
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(105)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106284C.1.pap
; US-10-425-115-191562

Query Match
Best Local Similarity 58.1%; Score 36; DB 16; Length 105;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTSESQ 12
DB 52 GMETLAPSHESQ 63

RESULT 22
US-10-264-049-2676
; Sequence 2676, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2676
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-049-2676

Query Match
Best Local Similarity 58.1%; Score 36; DB 15; Length 126;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTSESQ 12
DB 102 GVPSIPQTHSPQ 113

RESULT 23
US-10-425-114-68790
; Sequence 68790, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
```

```
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68790
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17018C01_FLI.pep
US-10-425-114-68790

Query Match          58.1%; Score 36; DB 15; Length 141;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 LPRTHESQ 12
DB      1 LPRTHESQ 8

RESULT 24
US-10-425-115-303972
; Sequence 303972, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 303972
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(150)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_40293C.1.pep
US-10-425-115-303972

Query Match          58.1%; Score 36; DB 16; Length 150;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 IEALPRT 9
DB      105 VEALPRVH 112

RESULT 25
US-10-282-122A-49712
; Sequence 49712, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
```

```
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 60191,078
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49712
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49712

Query Match          58.1%; Score 36; DB 15; Length 336;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 GIEALPRTHE 10
DB      146 GVEIRPREHQ 155

RESULT 26
US-10-739-930-7940
; Sequence 7940, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7940
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C32089_2.P
US-10-739-930-7940

Query Match          58.1%; Score 36; DB 16; Length 398;
Best Local Similarity 54.5%; Pred. No. 4.8e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 IEALPRTHEQ 12
DB      146 GVEIRPREHQ 155
```

Db 51 VASPRTHPSQ 61

RESULT 27  
US-10-369-493-11658

; Sequence 11658, Application US/10369493  
; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 11658

; LENGTH: 403

; TYPE: PRT

; ORGANISM: Agrobacterium tumefaciens

US-10-369-493-11658

Query Match 58.1%; Score 36; DB 15; Length 403;  
Best Local Similarity 70.0%; Pred. No. 4.9e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEALPRTTHS 11

Db 130 ITGLPRNHES 139

RESULT 28

US-10-369-493-14548

; Sequence 14548, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 14548

; LENGTH: 403

; TYPE: PRT

; ORGANISM: Agrobacterium tumefaciens

US-10-369-493-14548

Query Match 58.1%; Score 36; DB 15; Length 403;  
Best Local Similarity 70.0%; Pred. No. 4.9e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEALPRTTHS 11

Db 130 ITGLPRNHES 139

RESULT 29

US-10-369-493-15116

; Sequence 15116, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 15116

; LENGTH: 403

; TYPE: PRT

; ORGANISM: Agrobacterium tumefaciens

US-10-369-493-15116

Query Match 58.1%; Score 36; DB 15; Length 403;  
Best Local Similarity 70.0%; Pred. No. 4.9e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEALPRTTHS 11

Db 130 ITGLPRNHES 139

RESULT 30

US-10-425-115-269700

; Sequence 269700, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 269700

; LENGTH: 423

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_177563C.1.pcp

US-10-425-115-269700

Query Match 58.1%; Score 36; DB 16; Length 423;  
Best Local Similarity 54.5%; Pred. No. 5.2e+02;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEALPRTTHS 12

Db 41 VASPRTHPSQ 51

Search completed: August 1, 2005, 09:01:52  
Job time : 157 secs

**This Page Blank (uspto)**